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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

protein - protein database search, using Smith-Waterman algorithm MPsrch_pp

Mon Sep 13 14:25:32 1999; MasPar time 9.62 Seconds 433.103 Million cell updates/sec Run on:

Tabular output not generated.

>US-09-272-809-9 (1-196) from US09272809.pep 1458

1 KLAVRAISRLQSLPGGDIGA.........QAFGLQLQMELQLASQLAEK 196 Description: Perfect Score: Sequence:

PAM 150 Gap 11 Scoring table:

170751 seqs, 21266608 residues Sectrched:

Minimum Match 0% Listing first 45 summaries Post-processing:

Dulubase:

a-geneseq35
l:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part11 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26 27:part27 28:part28
29:part29 30:part30 31:part31 32:part32 33:part33
34:part34 35:part35 36:part36 37:part37 38:part38

Mean 31.852; Variance 133.240; scale 0.239 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Pred. No.	7.36e-89	1.58e-70	1.50e-27	2.65e+00	4.51e+00	1.53e + 01	2.57e+01	3.04e+01	3.04e+01	3.60e+01	5.05e+01	5.05e+01	5.05e+01	5.05e+01	5.05e+01	5.05e+01
	Description	Mesotaenium caldarior	Oat phytochrome A apo	Cyanobacterial phytoc	Sequence of human inh	Sequence of inhibin b	Cobra venom protease		Cobra venom protease	Cobra venom mocarhagi	Human growth hormone	Amino acid sequence o	Human poly-immunoglob	Rabbit seletal muscle	Rabbit calcium channe	Rabbit skeletal calci	Rabbit skeletal calci
	ID	W50145	W50144	W50143	P70204	P70852	W73007	P70201	W73009	W73013	P81326	W28089	W03178	P95645	W18390	W37711	R73055
	DB	32	32	32	7	~	37	~	37	37	П	31	20	П	22	26	13
	Query Match Length DB	1142	1129	748	353	91	621	351	613	621	638	236	746	1873	1873	1873	1873
æ	Query	6.69	57.4	27.6	7.1	6.9	6.4	6.2	6.2	6.2	6.1	0.9	9.0	0.9	0.9	9.0	0.9
	Score	1019	837	403	104	101	94	91	00	90	83	87	87	87	87	87	87
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WD-40 domain-contg. h WD-40 domain-contg. h Receptor of activated	x9 owt	h hormon	ochrome P4	ORF 3 of IgG light ch	cytochrome	υ		Human auxillary cytoc	Human auxillary cytoc	ved cy	H	chrome P45		Delta-pyrroline-5-car	Deltal-pyrroline-5-ca	Rice delta-1-pyrrolin	Acetobacter diguanyla	Rabbit ATHERO-ELAM.	Streptomyces venezuel	H. pylori transporter	71	¥	-128 kilod	Helicobacter pylori T
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ALIGNMENTS

1 KLAVRAISRLQSLPGGDIGALCDTVVEDVQRLTGYDRVMVYQFHEDDHGEVVSEIRRSDL

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This polypeptide comprises phytochrome A (PHYA) of oat. A method for the efficient purification of recombinant PHYA from Saccharomyces cerevisiae using a C-terminal epitope tag is provided. The invention provides a new class of fluorescent provides a new class phycocrythrobilin. Preferred apoproteins are obtained from plants, e.g. oats, from green algae, e.g. Mesotaenium caldariorum (see W50145), or from green algae, e.g. Mesotaenium caldariorum (see W50145), or from cyanobacteria such as.Sprechocystis (see W50143). Truncated apoproteins consisting of the N-terminal chromophore domain are specially preferred. Recombinant apoproteins assemble spontaneously with the bilin chromophore. Claimed compositions comprise a protein, glycoprotein, antibody or nucleic acid to be detected linked to the fluorescent adduct. They are used in assays for detecting the other member of a specific binding pair, e.g. immunoassay of antigens, immuno-histochemical labelling, as nucleic acid probes for Southern blotting, for identification of manufactured products, also to detect protein protein interactions, including studies on intracellular protein localisation and identification of transfactors.
                                                                                        'n
                                                                                                                                                                                                                                                                                                     382
                                                                                                                                                                                                                                       203 klaakaisrlqslpggdigllcdavveevreltgydrvmaykfhedehgeviaeirrsdl 262
                                                                                                                                                                                                               263 epylglhypatdipqaarflfmknrvriicdcsappvkvigdptmkhpislagstlrgvh 322
                                                                                                                                                                       9
                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Adducts of apoprotein polypeptide and chromophore as label, particularly for bio-molecules - used as fluorescent markers in immunoassays, nucleic acid hybridisation, detecting protein interaction etc., are stable with high molar absorption Example 1; Page 63: 87pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 837; DB 32; Length 1129;
Pred. No. 1.58e-70;
32; Mismatches 36; Indels 15; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         transfected cells. The phytofluors make ideal fluorescent markers because they have a long wavelength absorption maximum and high molar absorption coefficient, and are stable to light and pH.
                                                                                                                                                   gchaqymanmgsvaslvmaviindnsseegataaggilhkgrklwglvvchhsspryvpf
                                       Score 1019; DB 32; Length 1142;
Pred. No. 7.36e-89;
28; Mismatches 22; Indels 14;
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Oat phytochrome A apoprotein.
Phytofluor; fluorescent label; phytochrome A; oat.
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W50144 standard; protein; 1129
                                       69.9%;
ilarity 69.5%;
Conservative
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Best Local Similarity 60.7%;
Matches 128; Conservative
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01-AUG-1997; U13529.
02-AUG-1996; US-023217.
(REGC ) UNIV CALIFORNIA.
Lagarias JC, Murphy JT;
WPI; 98-145711/13.
1142 AA;
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Matches 146; Conser
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WO9805944-Al.
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Adducts of apportein polypeptide and chromophore as label,

That particularly for bio-molecules - used as fluorescent markers in immunoassays, nucleic acid hybridisation, detecting protein-protein interaction etc., are stable with high molar absorption

Example 4, Fig 10B; 87pp; English.

C This polypeptide comprises cyanobacterial phytochrome 1 (Cphl) of Synchocystis sp. PCC6803. Its amino acid sequence was deduced from locus slr0473 genomic DNA. Expression of the 748-residue comprises of protein adduct with a red, far-red photoreversible phytochrome signature. The invention provides a new class of fluorescent component con use as fluorescent markers. They comprise a protein component can apoprotein) and a bilin chromophore such as phycocrythrobilin.

C Perferred apoproteins are obtained from plants, e.g. oats (see
                                                                        especially preferred. Recombinant apoproteins assemble sportaneously with the bilin chromophore. Claimed compositions comprise a protein, glycoprotein, antibody or nucleic acid to be detected linked to the fluorescent adduct. They are used in assays for detecting the other member of a specific binding pair, e.g. immunoassay of antigens, immuno-histochemical labelling, as nucleic acid probes for Southern blotting, for identification of manufactured products, also to detect protein-protein interactions, including
                   61 EPYLGLHYPATDIPQAARFLEKQNRVRMICDCNATPVKVVQSEELKRPLCLVNSTLRAPH 120
                                                                                                            ----KLWGLVVGHHCSPRYVP 165
 epylglhypatdipqaarllfmknkvrmicdcrarsikvieaealpfdislcgsalraph
                                                                                                                                                                                                                                                                                                           Cyanobacterial phytochrome Cph1 apoprotein.
Phytofluor; fluorescent label; phytochrome; Cph1; cyanobacterium.
Synechocystis sp. strain PCC6803.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          W50144), from green algae, e.g. Mesotaenium caldariorum (see W50145), or cyanobacteria such as Synechocystis. Truncated apoproteins consisting of the N-terminal chromophore domain are
                                                                                                                                                                                                                                                                                                                                                                                                    /note= "undetermined amino acid residue"
536.544
/note= "histidine kinase transmitter module
conserved motif"
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conserved motif"
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conserved motif"
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                                                                                                          121 GCHTQYMANMGSVASLALAIVVKGK---D---S---S-
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                                                                                                                                                                                                                                                         W50143 standard; protein; 748 AA.
W50143;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       02-AUG-1996; US-023217.
(REGC ) UNIV CALIFORNIA.
Lagarias JC, Murphy JT;
WPI; 98-145711/13.
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201 cqelavvpvfvdpgeeshrpfvvvqarl 228
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02-OCT-1986; 307586.
03-OCT-1985; US-783910.
10-FEB-1986; US-827710.
12-SEP-1986; US-906729.
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18-FEB-1998; US-026001.
15-APR-1997; US-843373.
23-JAN-1998; US-012637.
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WPI; 98-568735/48
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Pred. No. 2.65e+00;
19; Mismatches 27; Indels 11; Gaps 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   manaalnr1rg-ga-n1rdfydviveevrrm1qfgrvm1yrrdennhcdv1a1dkrddme 196
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studies on intracellular protein localisation and identification of transfected cells. The phytofluors make ideal fluorescent markers because they have a long wavelength absorption maximum and high molar absorption coefficient, and are stable to light and pH. Sequence 748 AA;
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//note="used to design a long synthetic DNA probe"
238..237
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/note="potential N-linked glycosylation sites"
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Sequence of human inhibin beta-chain precursor beta-B
Fertility control; contraception; hormone; spermatogenesis.
Homo saplens.
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                                                                                                                                                                                                                                                                                                     Score 403; DB 32; Length 74
Pred. No. 1.50e-27;
51; Mismatches 49; Indels
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/note-"proteolytic processing site"
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P70204 standard; protein; 353 AA.
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Best Local Similarity 35.2%;
Matches 31; Conservative
                                                                                                                                                                                                                                                                                                     Query Match 27.6%;
Best Local Similarity 36.5%;
Matches 62; Conservative
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10-FEB-1986; US-827710.
12-SEP-1986; US-906729.
(GETH ) GENENTECH INC.
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WPI; 87-137512/20.
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02-OCT-1986; 307586
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셤 ò

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2 rvkvy-fqeqghgdrwnmvekrvdlkrs-gwhtfplteaiqal-fergelnlsvqcdscq 58
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Mocarhagin; snake venom; Mocambiquan spitting cobra; protease; inflammation; myocardial infarction; thrombosis; infection; metaatasis; therapy; NMM-1.
Naja mossambica mossambica.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fertility control; contraception; hormone; spermatogenesis EP-222491-A.
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Sequence of inhibin beta-B chain prodomain
(GEMY ) GENETICS INST INC.

Boodhoo A, Sako D, Seehra JS, Shaw G;
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24..621
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W73007 standard; Protein; 621 AA.
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                                                                                                                                                                                                                                                                               T 5
P70852 standard; protein; 91
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        it isolated mocarhagin cobra venom protease, and nucleic acids encoding it isolated mocarhagin cobra venom protease, and nucleic acids encoding it isolated mocarhagin broducts for treating e.g. myocardial infarction, thrombosis, bacterial or viral infection, metastatic conditions or inflammatory disorders

Claim 21; Page 35-38; 97pp; English.

Claim 21; Page 35-38; 97pp; English.

This is the amino acid sequence of mocarhagin NAM-1, a highly specific metalloproteinase from the venom of the Mozambiquan specific metalloproteinase from the venom of the Mozambiquan spitting cobra. The invention provides mocarhagin polypeptides

Csee W33007-13) and polynucleotides (see V7895-90) encoding them, as well as host cells and methods of producing the (especially mature) polypeptide containing sulphated tyrosine residues, p-selectin glycoprotein (GP) ligand. (PSGL-1) and GDIb-alpha (claimed). They also inhibit neutrophil/Hu60 binding, inhibit colorentrations of DPP (claimed). They can be used to inhibit in concentrations of DPP (claimed). They can be used to inhibit selectin-mediated binding and to treat inflammatory disease
                                                                                                                                                                                                                                                                                       claimed). In particular, they can be used to treat e.g. myocardial infartion, metastatic conditions, inflammatory discressed infartion, metastatic conditions, inflammatory discress such as artheritis, acute respiratory distress syndrome, asthma, emphysema, delayed type hypersensitivity reaction, systemic lupus erythermatosus, thermal injury such as burns or frostbite, autoimmune thyroiditis, experimental allergic encephalomyelitis, autoimmune thyroiditis, experimental allergic encephalomyelitis, multiple sclerosis, multiple organ injury syndrome secondary to trauma, diabetes, Reynaud's syndrome, neutrophilic dermatosis (Sweet's Syndrome), inflammatory bowel disease, Grave's disease, glometulonephritis, gingivitis, periodontitis, haemolytic uremic syndrome, ulcerative colitis, crohn's disease, necrotising creterocolitis, granulocyte transfusion associated syndrome, cytokine-induced toxicity. Mocarhagin protein may also be useful in organ transplant rejection, to treat transplantation and to quell organ transplant rejection, to treat the amendialysis and leukophoresis pattents, or as an inhibitor of process.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'note "used to design a long synthetic DNA probe"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      39 vpalskggvqnpqpetkyedtmqyefhvngepvvlhlernkglfsedytethyap 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         09-APR-1991 (first entry) sequence of porcine inhibin beta-chain precursor beta-B. Settility control; contraception; hormone; spermatogenesis. Sus scrofa domestica.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; N70318.
Recombinant human or porcine inhibin or activin - used for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 621;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 94; DB 37; Length 621;
Pred. No. 1.53e+01;
9; Mismatches 27; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="proteolytic processing site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                P70201 standard; protein; 351 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 6.4%;
Best Local Similarity 30.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20-MAY-1987.
02-OCT-1986; 307586.
03-OCT-1985; US-783910.
10-FEB-1986; US-9827710.
12-SEP-1986; US-9067729.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          271..386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mason AJ, Seeburg PH; WPI; 87-137512/20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cleavage_site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EP-222491-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            region
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Score 91; DB 2; Length 351;
Pred. No. 2.57e+01;
16; Mismatches 30; Indels 11; Gaps 11;
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Claim 40; Page 45-48; 97pp; Engglish.

This is the amino acid sequence of mocarhagin NMM-9, a highly specific metalloproteinase from the venom of the Mozambaquan specific metalloproteinase from the venom of the Mozambaquan specific metalloproteinase from the venom of the Mozambaquan splitting cobra. The invention provides mocarhagin polypeptides (see W73007-13) and polynucleotides (see W7895-901) encoding them, sa well as host cells and methods of producing the (especially mature) polypeptides. Mocarhagin proteins are capable of cleaving anionic polypeptide containing sulphated tyrosine residues,

P-selectin glycoprotein (GP) ligand-1 (PSGL-1) and GPlb-alpha containing to von Willebrand Factor, require Ca2+ and Zn2+ ions for activity and have activity inhibited by excess EDTA or concentrations of DPP (claimed). They can be used to inhibit selectin-mediated binding and to treat inflammatory disease (claimed). In particular, they can be used to treat e.g. myocardial infarction, vessel restenosis, thrombosis, bacterial or viral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            140 rvkvy-fqepghgdrwdvvekrvdlkrs-gwhtlplteaiqal-fergerrlnldvqcdg 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ||:|| |:| |: : : : | | | : : : || | 37 RVMVYQFHEDDHGEVVSEI-RRSDLEPYLGLH-YPATDIPQAARFLFKQNRVRM-I-CD-91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Isolated mocarhagin cobra venom protease, and nucleic acids encoding
                                                                 Disclosure; Fig 2B; 48pp; English.
A compsn. comprising human or porcine inhibin which is completely free of unidentified or porcine proteins is claimed. Also claimed are non chromosomal DNA encoding inhibin-alpha or an inhibin-beta chain. Sequencing of inhibin-encoding cDNA has led to the identification of prodomain regions located N-terminal to the mature inhibin chains that represent coordinately expressed
                                                                                                                                                                                                                                                                                                                                                   biologically active polypeptides. The prodomain regions or prodomain immunosens are useful in monitoring preproinhibin processing in transformant cell culture or in experiments directed at modulating the climical condt. or reproductive physiology of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cobra venom professe mocarhagin NMM-9.
Mocarhagin; snake venom; Mozambiquan spitting cobra; protease; inflammation; myocardial infarction; thrombosis; infection; metastasis; therapy; NMM-9.
Naja mossambica mossambica.
modulating clinical condition or reproductive physiology of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     92 CNA-TPVKV-VQS-EELKRPLCLVNSTL 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                197 cgelavvpvfvdpgeeshrpfvvvgarl 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Boodhoo A, Sako D, Seehra JS, Shaw G;
WPI; 98-568735/48.
N-PSDB; V07897.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /label= Sig_peptide
24..613
/label= Mat_protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     W73009 standard; Protein; 613 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity 35.2%;
les 31; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              02-FEB-1999 (first entry)
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15-APR-1997; US-843373.
23-JAN-1998; US-012637.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4-APR-1998; U07998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       351 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  animals.
                                            animals.
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if - used to develop products for treating e.g. myocardial
infarction, thrombosis, bacterial or viral infection, metastatic
conditions or inflammatory disorders
Claim 80; Page 65-68; 97pp; English.
This is the amino acid sequence of a modified cobra venom mocarhagin
This is the amino acid sequence of a modified cobra venom mocarhagin
Cream 100 protein, termed NMM-9ek, that includes an enterokinase cleavage site
between the propeptide and mature peptide of mocarhagin (see also
W73009). Introduction of the cleavage site may allow secretion of
active mocarhagin from eukaryotic host cells. The invention
provides mocarhagin polypeptides (see W73007-13) and polymucleotides
(see V07895-901), as well as host cells and methods of producing
(sepecially mature) polypeptide containing sulphated tyrosine
residues, P-selecting plycoprotein (GP) ligand-1 (PSGL-1) and
cellawing anionic polypeptide containing sulphated tyrosine
residues, P-selecting plycoprotein (GP) ligand-1 (PSGL-1) and
GPID-alpha (claimed). They also inhibit neutrophil/HL60 binding,
inhibit platelet binding to von Willebrand Factor, require Ca2+ and
Zn2+ ions for activity and have activity inhibited by excess EDTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1;
                                                                                                crytematosus, thermal injury such as burns or frostbite, autoimmune thyroiditis, experimental allergic encephalomyelitis, autitiple organ injury syndrome secondary to trauma, diabetes, Reynaud's syndrome, neutrophilic dermatosis (Sweet's syndrome), inflammatory bowel disease, Grave's disease, glomerulonephritis, gingivitis, periodonitis, haemolytic uremic syndrome, ulcerative colitis, crohn's disease, necrotising entercolitis, granulocyte transfusion associated syndrome, cytokine-induced entercolitis, granulocyte transfusion associated syndrome, or cytokine-induced toxicity. Mocarhagin protein may transplantation, both to prepare organs for transplantation and to quell organ transplant rejection, to treat transplantation and to quell organ transplant rejection, to treat haemodialysis and leukophoresis patients, or as an inhibitor of Perecolar organs or Presentin-mediated intercellular adhesion.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
infection, metastatic conditions, inflammatory disorders such as arthritis, acute respiratory distress syndrome, asthma, emphysema delayed type hypersensitivity reaction, systemic lupus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 39 vpalskggvqnpqpetkyedtmqyefqvngepvvlhlernkglfsedytethyas 93
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         spitting cobra; proteathrombosis; infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 613;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 90; DB 37; Length 613
Pred. No. 3.04e+01;
10; Mismatches 27; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            192..196
/note= "enterokinase cleavage site"
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WPI; 98-568735/48.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mocarhagin; snake venom; Mozambiquan
inflammation; myocardial infarction;
metastass; therapy; NMM-9ek.
Naja mossambica mossambica.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /label= Pro_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 197..021
/label- Mat_protein
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W73013 standard; Protein; 621 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cobra venom mocarhagin NMM-9ek
Mocarhagin; snake venom; Mozamk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 6.2%;
Best Local Similarity 29.1%;
Matches 16; Conservative
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18-FEB-1998; US-026001.
15-APR-1997; US-843373.
23-JAN-1998; US-012637.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 613 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cleavage_site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
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or high concentrations of DFP (claimed). They can be used for inflammatory disease (claimed). In particular, they can be used for treating e.g. myocardial infarction, vessel restenosis, thrombosis, bacterial or viral infarction, wessel restenosis, thrombosis, bacterial or viral infection, metastatic conditions, inflammatory discretes such as arthritis, acute respiratory distress such as arthritis, acute respiratory distress such as arthritis, acute respiratory distress such as arthritis, acute respiratory distress. Systemic lupus erythematosus, thermal injury e.g. burns or frostbite, autoimmune thyroiditis, experimental allergic encephalomyelitis, autoimmune thyroiditis, multiple organ injury syndrome secondary to trauma, diabetes, Reynaud's syndrome, neutrophilic dermatosis (Sweet's syndrome), inflammatory bowel disease, Grave's disease, glomerulonephritis, gingivitis, periodontitis, memolytic uremic syndrome, ulcerative colitis, Crohn's disease, necrotising enterocolitis, granulocyte transfusion associated syndrome, or cytokine-induced toxicity. Mocarhagin protein may also be useful in organ transplant rejection, to treat transplantation and to quell organ transplant rejection, to treat transplantation and to quell organ transplant rejection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 285 flfskqqrikmlslppvpvpkikgidpdllkegkleevntilaihdsykpefhsddswve 344
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The sequence was deduced from a clone isolated from an adult liver cDNA lambda gt10 library. The DNA can be inserted into an expression vector for prodn. of the recombinant GHR which is used to treat GH-related disorders such as gigantism and acromegaly. A hydropathy plot revealed an extracellular GH binding domain, a transmembrane domain, and an intracellular signalling domain. Eight potential N-linked glycosylation sites are predicted.

See also PB1327 and NB1718-9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New pure growth hormone receptor and binding protein - for treating growth hormone abnormalities, and new encoding DNA sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                               haemodialysis and leukophoresis patients, or as an inhibitor of Portselectin-mediated intercellular adhesion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           39 vpalskggvqnpqpetkyedtmqyefqvngepvvlhlernkglfsedytethyas 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18 IGALCDIVVEDVQRLTGYDRVMYYQFHEDDHGEVVSEIRRSDL--EPYLGLHYPA 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 37; Length 621;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 90; DB 37; Length 621;
Pred. No. 3.04e+01;
10; Mismatches 27; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 638;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23-0CT-1990 (first entry)
Human growth hormone receptor.
Growth hormone receptor; gigantism; acromegaly.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 89; DB 1; L
Pred. No. 3.60e+01;
17; Mismatches 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hammonds RG, Leungh DW, Spencer SA, Wood WI; WPI; 88-368632/51.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
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P81326 standard; protein; 638 АА.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 6.2%;
Best Local Similarity 29.1%;
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 6.1%;
Best Local Similarity 27.3%;
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            L2-JUN-1987; US-062542.
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10-JUN-1988; U02008.
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New DNA encoding alpha-2 subunit of animal calcium channel - also new
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          plants - useful for passive immunisation against mucosal antigens, esp. against S. mutans and S. sorbinus to prevent dental caries Disclosure; pages 105-108; 152pp; English.

The present sequence is the human poly immunoglobulin (Ig) receptor, a portion of which corresp to residues 1-67, pref. 1-606, or esp. residues 13-45, 1-120, 110-230, 210-340, 320-450, A40-550, 550-606 or 550-657 comprises a protection protein (PP). The Ig of the invention comprises a PP as above in association with an Ig derived heavy chain, having at least a portion of an antigen (Ag) binding domain. The PP protects the Ig in harsh mucosal, e.g. gastrointestinal, environments, therefore enhancing its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          effectiveness in passively immunishing animals against nucosal pathogens. The Ag binding domain is specifically derived from the Guy's 13 antibody, and the Ig can be used to prevent dental caries by binding, e.g. Streptococcus mutans serotypes c, e and f, or serotinus serotypes d and g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Immunoglobulin and protection protein complex and its prodn. in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   258 gencdvvvntlgkrapafegrillnpqdkdgsfsvvitglrkedagrylcgah 310
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04-APR-1988; 001408.
04-APR-1988; US-176699.
(SALK) Salk Inst for Biol Stud.
Ellis SB, Williams ME, Harpold MM, Schwartz A, Sartor J; WPI: 89-124236/44.
                                                                                                                                                                                                                                      "external portions of domain VI"
                                                                                                                                                                                                                                                                                domain
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                                                                                                                                                                                                                                                                                                                        /label = transmembrane_segment
                                                                                                                                                                                                                                                                                                                                                         /label= intracellular_portion
                                                                                                                                                                                                                                                                              "external portions of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SCHOOLS GUYS
                                                                                                          domain_III
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P95645 standard; protein; 1873 AA.
P95645;
                                            110..230
/label- domain_II
                                                                                                                                                    /label- domain_IV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (PLAN.) PLANT BIOTECHNOLOGY INC. (UNME-) UNITED MEDICAL & DENTAL S (PLAN-) PLANET BIOTECHNOLOGY INC. Hiatt AC, Lehner T, Ma JKC; WPI; 96-333387/33.
                                                                                                                                                                                            domain_V
                          'label= domain_I
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Best Local Similarity 28.3%;
Matches 15; Conservative
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27-DEC-1995; U16889.
30-DEC-1994; US-367395.
04-MAY-1995; US-434000.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present sequence represents a Staphylococcus aureus protein, that, based on homology with a Bacillus subtilis protein, is believed to be a DNA repeir protein RECN (recombination protein N). The DNA sequence was isolated from a library of clones of S. aureus WCHH 29 in Escherichia antisense sequence can be used in the construction of ribozymes and antisense sequences to control the expression of Staphylococcal genes. The DNA sequence is also useful as a source of regulatory elements for the control of bacterial gene expression. The present protein may be used to produce vaccines to enable a host to produce specific antibodies with antibacterial action. These vaccines and antibodies would protect a host against invasion by S. aureus, and conditions relating to Staphylococcal infection, e.g. Staphylococcal food poisoning, scaled skin syndrome, and toxic shock syndrome.
                                                                                                                   Amino acid sequence of DNA repair protein RECN (recombination protein N). Staphylococcus aureus protein; ribozyme; antisense sequence; control; Staphylococcal gene; regulatory element; bacterial gene expression; vaccine; staphylococcal infection; food poisoning; scaled skin syndrome;
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the specification"
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W03178;
424-FEB-1997 (first entry)
Human poly-immunoglobulin receptor.
Human; immunoglobulin; receptor; protection protein; mutans;
heavy chain; antigen binding domain; protection; pathogen;
mucosal; environment; gastrointestinal; passive; immunisation;
Guy's 13 antibody; prevention; dental caries; Streptococcus;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel polypeptide(s) from Staphylococcus aureus strain WCUH29 to isolate antimicrobial compounds, and in vaccines against S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Black MT, Burnham MK, Hodgson JE, Knowles DJC, Nicholas RO,
Pratt JM, Reichard RW, Rosenberg M, Ward JM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 87; DB 31; Length 236;
Pred. No. 5.05e+01;
22; Mismatches 30; Indels
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                                                         .T 11.
W28089 standard; Protein; 236 AA.
                                                                                                                                                                                                                                                                                                                                                                                    21-AUG-1997.
19-FEB-1997, UO2318.
20-FEB-1996; US-011888.
(SMIK ) SMITHKLINE BEECHAM CORP.
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Best Local Similarity 23.9%;
Matches 17; Conservative
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                                                                                                                                                                                                                                                        Staphylococcus aureus
                                                                                                                                                                                                                                    toxic shock syndrome.
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135 SLALAI 140
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Best Local
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t or antagonist activity
closure; page 16-1 to 18-3; 68pp;
siso used to diagnose Lambert-Eaton s
with alpha-1 and alpha-2 subunits. L
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Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    transformation;
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Similarity 35.4%;
17; Conservative
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um channel alpha-1 subunit.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    nuscle; calcium Channel; alpha-2; subunit; alpha-1; reporter gene; screening assay; agonist; antagonist.
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79
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257
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687
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637..6
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    /note= "Tr.
1153..1172
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1119..1137
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Pred.
8; N
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No. 5.05e+01;
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ban be used a
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alpha-1 subunit. This protein comprises twenty-four potential transmembrane regions and has a molecular weight of 212143. The protein contains four internal repeated segments. Each repeat the protein contains four internal repeated segment with strong comprises five hydrophobic segments and one segment with strong positive charge. The alpha-1 protein lacks a hydrophobic amino positive charge characteristic of a signal peptide and it is compared that the four internal repeats represent the 24 transmembrane thought that the four internal repeats represent the 24 transmembrane compared that the rough conjunction with the alpha-2 subunit coding segments and that the N- and C-termini are extracellular. This sequence (see also T70227) to transform a eukaryotic cell. The cell case quence (see also T70227) to transform a eukaryotic cell. The cell case used optionally with a reporter gene, in screening assays for case channel agonists or antagonists.
RESULT
ID W:
AC W:
DT 1:
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KW R
KW P
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04-APR-1989; 1
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Brenner R, Ellis SB, Harpo
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N-PSDB; T70228.
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                        W37711 standard; Protein; J
W37711;
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Rabbit; skeletal; Calcium
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17; Conservative
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PT suburits

PS Disclosure; Fig 1A-J; 44pp; English.

CC This is a rabbit skeletal muscle calcium channel alpha-1 subunit.

CC The DNA sequences of the alpha-2 subunit (rabbit and human - 196812-13) are useful as hybridisation probes for identifying nucleic conclusion of the second and the second and the second action of t
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                                                                                                                                              Query Match 6.0%; Score 87; DB 26; Length 1873; Best Local Similarity 35.4%; Pred. No. 5.05e+01; Matches 17; Conservative 8; Mismatches 20; Indels
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08-NOV-1990; US-503751.
04-APR-1988; US-776899.
04-APR-1988; WO-U01408.
13-UUL-1992; US-914231.
28-SEP-1994; US-914231.
28-SEP-1994; US-914083.
(SIBI-) SIBIA NEUROSCIENCES INC.
Brenner R, Ellis SB, Harpold MM, Schwartz A, Williams ME;
WPI; 97-S8134/51.
N-PSDB; T96811.
Oligonucleotide probes - for identifying calcium channel alpha-2
746 eedepeipvsprprplae-lqlkekavpipeassfflfsptnkvrvlc 792
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45 EDDHGEVVSEIRRSDLEPYLGLHYPATDIPQAARF-LFKQ-NRVRMIC 90
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US5686241-A.
11-NOV-1997.
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Search completed: Mon Sep 13 14:26:09 1999 Job time : 37 secs.

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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

MPsrch_pp protein - protein database search, using Smith-Waterman algorithm Mon Sep 13 14:24:55 1999; MasPar time 10.30 Seconds 762.567 Million cell updates/sec

Tabular output not generated.

Run on:

>US-09-272-809-9 (1-196) from US09272809.pep 1458

Sequence: Description: Perfect Score: 1 KLAVRAISRLQSLPGGDIGA.....QAFGLQLQMELQLASQLAEK 196

Scoring table: PAM 150 Gap 11

Searched: 122810 seqs, 40068593 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

pir60 1:pir1 2:pir2 3:pir3 4:pir4

Statistics: Mean 44.061; Variance 81.846; scale 0.538

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	8	7	σ	υı	4	ω	2		Result No.
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ALIGNMENTS

Db 381	рь 321 Qy 121	Db 261 Qy 61	0b 201 0y 1	Query M Best Lo Matches	322 SUMMARY	CLASSIFICATION KEYWORDS FEATURE 63-569	##IC GENETICS #gene	#cross-ref #accession	#authors #journal #title	ACCESSIONS REFERENCE	RESULT ENTRY TITLE ORGANISM
LQLQMELQLASQLAEK 396 	1 GCHTQYMANMGSVASLALAIVVKGKDSSKLWGLVVGHHCSPRYVPFPLRYACEFLMQAFG 380 	EPYLGLHYPATDIPQAARELEKQNRVRMICDCNATPVKVVQSEELKRPLCLVNSTLRAPH 	KLAVRAISRLQSLPGGDIGALCDTVVEDVQRLTGYDRVMVYQFHEDDHGEVVSEIRRSDL 260 	Query Match 100.0%; Score 1458; DB 2; Length 1112; Best Local Similarity 100.0%; Pred. No. 9.32e-293; Matches 196; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	<pre>#binding_site phytochromobilin (Cys) (covalent) #status predicted #length 1112 #molecular-weight 122587 #checksum 9259</pre>	#supe phyto	##motoure 1-1112 ##label CLA ##rcross-references EMBL:X76610; NID:g452815; PID:g452817 CS PHYE	#cross-references MUID:94325466 #accession S46313 #accession DNA	rs Clack, T.; Mathews, S.; Sharrock, R.A. al C-Plant Mol. Biol. (1994) 25:413-427 The phytochrome apoprotein family in Arabidopsis is encoded by five genes: the sequences and expression of PHYD and PHYE.	01-May 1998 S \$46313; \$41912 S46312	1 S46313 #type complete phytochrome E - Arabidopsis thaliana #formal_name Arabidopsis thaliana #common_name mouse-ear press or_in_lost #sequence revision 27.Jan-1995 #text change

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181 LQLQMELQLASQLAEK

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ENTRY
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#journal Genes Dev. (1989) 3:1745-1757

#title Novel phytochrome sequences in Arabidopsis thaliana:

**Structure, evolution, and differential expression of the plant regulatory photoreceptor family.

#cross-references MUID:90108670
#accession
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                                                                                                                                    ##cross-references EMBL:X17342; NID:g16422; PID:g16423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     173
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 215 KLAVRAISHLQSLPGGDVKLLCDTVVESVRELTGYDRVMVYKFHEDEHGEVVAESKIPDL 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              **status preliminary; translated from GB/EMBL/DDBJ##molecule_type DNA
                                                                                                                                                           ##residues
                                                                                                                                                                            ##molecule_type mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GCHAQYMANMGSIASLTLAVIINGNDEEAVGGRSSMRLWGLVVGHHTSARCIPFPLRYAC 394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      78.4%;
nl Similarity 77.0%;
157; Conservation
                               Reed, J.W.; Nagpal, P.; Poole, D.S.; Furuya, M.; Chory, Plant Cell (193) 5:147-157
Mutations in the gene for the red/far-red light receptor phytochrome B alter cell elongation and physiological
                                                                                                                                                                                                                                                                                                                                                                                                                    FKMUB #type complete
phytochrome B - Arabidopsis thaliana
phytochrome B - Arabidopsis thaliana #common_name mouse-ear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      phyB superfamily phytochrome; phytochrome homology photoreceptor; phytochromobilin photoreceptor; which weight 125808 #checksum flength 1132 #molecular-weight 125808 #checksum
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kern, R.; Gasch, A.; Deak, M.; Kay, S.A.; Chua, N.H. Plant Physiol. (1993) 102:1363-1364
PhyB of tobacco, a new member of the photoreceptor f
                                                                                                                                                                                                     B33473
                                                                                                                                                                                                                                                                                                                                                             B33473; JQ2141; S07718
                                                                                                                                                                                                                                                                                                                                                                                                     30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change
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phytochrome B - common tobacco
#formal_name Nicotiana tabacum #common_name common tobacco
24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change
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                                                                                                                                                         1-1172 ##label SHA
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Pred. No. 1.65e-221;
25; Mismatches 14;
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901-1172
357
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103-623
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                                                                                                                                                                                                                                                                                                                                                #authors Dehesh, K.; Tepperman, J.; Christensen, A.H.; Quail, #journal Mol. Gen. Genet. (1991) 225:305-313 #title phyB is evolutionarily conserved and constitutively in rice seedling shoots.
                                                                                                                                                                     364
                                                                                                                                                                                                                                                                                                                                      #accession
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                                                                                                                                                                                                                                                                                 ##molecule_type DNA
##residues 1-1171 ##label
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          170
             243 KLVVRAISRLQALPGGDVKLLCDTVVEHVRELTGYDRVMVYRFHEDEHGEVVAESRRSNL 302
                                                                                                                                                                                                                                                                                                                      ##status
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ##experimental_source ecotype Landsberg,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ##residues 1-1172 ##label REE
##cross-references GB:L09262
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##residues 1-1
                                                                                  Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GCHTQYMANMGSVASLALAIVVKGK--D-----SS-KLWGLVVGHHCSPRYVPFPLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        YACEFLMQAFGLQLQMELQLASQLAEK 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GCHSQYMANMGSTASLAMAVIINGNEDDGSNVASGRSSMRLWGLVVCHHTSSRCIPFPLR 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EPYLGLHYPATDIPQAARFLFKQNRVRMICDCNATPVKVVQSEELKRPLCLVNSTLRAPH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KLAVRAISQLQALPGGDIKLLCDTVVESVRDLTGYDRVMVYKFHEDEHGEVVAESKRDDL 295
                                                         73.1%;
l Similarity 72.7%;
152; Conservation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         h 73.4%;
Similarity 73.9%;
l53; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                      S14065
S14065
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 $14065  #type complete
phytochrome B - rice
#formal_name Oryza sativa #common_name rice
19-Mar-1997  #sequence_revision 19-Mar-1997  #text_change
                                                                                                                                                                                                               phyB
#superfamily phytochrome; phytochrome homology
photoreceptor; phytochromobilin; transcription
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722/1; 991/2; 1088/2
#superfamily phytochrome;
dimer; photoreceptor; phyt
                                                                                                                                 #length
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                                                                                                                                                                #domain phytochrome homology #label PHYT\
#binding_site phytochromobilin (Cys) (covalent) #status
                                                                                                                                                                                                                                                                                                                    preliminary
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#domain signal transduction #label STD\
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1171 #molecular-weight 128384
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                                                              Pred.
23; 1
                                                                                Score 1066; DB 2;
Pred. No. 3.40e-204;
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Pred. No. 4.30e-205;
25; Mismatches 18;
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                                                                                               Length 1171;
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KLAVRAISRLQSLPGGDIGALCDTVVEDVQRLTGYDRVMVYQFHEDDHGEVVSEIRRSDL

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FEATURE
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  Query Match
Best Local Similarity
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*cross-references MUID:98121113

*accession B71429

*#statue
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#title
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                                                                                                                                                                                                                                                                                                                                                            #cross-references MUID: 94325466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   #authors
                                                                                                                                                                                                                                        #gene
                                                                                                                                                                                                                                                                       ##molecule_type DNA
##residues 1-424,'F',426-1164 ##label CLA
##cross-references EMBL:X76609; NID:g452812; PID:g452814
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##cross-references GB:Z97340; NID:g2244950; PID:e326982;
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Kavanagh, T.; Hempel, S.; Kotter, P.; Entian, K.D.; Rieger,
M.; Schaeffer, M.; Funk, B.; Mueller-Auer, S.; Silvey, M.;
James, R.; Montfort, A.; Pons, A.; Pulydomenech, P.; Douka,
A.; Voukelatou, E.; Milioni, D.; Hatzopoulos, P.;
Piravandi, E.; Obermaier, B.; Hilbert, H.; Duesterhoft, A.;
Moores, T.; Jones, J.D.G.; Enewa, T.; Palme, K.; Benes, V.;
Rechman, S.; Ansorge, W.; Cooke, R.; Berger, C.; Delseny,
M.; Voet, M.; Volckaert, G.; Mewes, H.W.; Klosterman, S.;
Schueller, C.; Chalwatzis, N.
Nature (1998) 391:485-488
Analysis of 1.9 Mb of contiguous sequence from chromosome 4
                                                                                                                                            4COP9-4G3845
#superfamily phytochrome; phytochrome homology bhotoreceptor; phytochromobilin; transcription
                                                                                                                                                                                                                                                                                                                                                                                                  SA6312 Clack, T.; Mathews, S.; Sharrock, R.A. Plant Mol. Biol. (1994) 25:413-427 The phytochrome apoprotein family in Arabidopsis for the fire and expression of
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                                                                 #length
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#formal_name
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PHYE.
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                                                                                                    #domain phytochrome homology #!
#binding_site phytochromobilin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            preliminary; nucleic acid sequence
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  71.3%;
71.6%;
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D - Arabidopsis thaliana
ne Arabidopsis thaliana #common_name
                                                               #molecular-weight 129267
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  3.90e-198;
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                                                                                                                                                                                                                                                                                                              258 EPYLGLHYPATDIPQASRFLFMKNRVRVIADCCASPVKLIQDPDIKQPVSLAGSTLRAPH 317
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IFICATION #superfamily phytochrome; phytochrome
phytochromobilin
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                                                                                                                                                                                                                                                                                                                                                                                                                                            n 70.6%;
Similarity 69.3%;
01-May-1998
S28431
S28431
                                            $28431 #type complete
phytochrome B - potato
#formal_name Solanum tuberosum
07-May-1993 #sequence_revision
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          predicted #length 577 #che
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hughes, J.; Mittmann, F. submitted to the EMBL Data Library, July 1995 The moss Ceratodon purpureus contains and exp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        phytochrome - moss (Ceratodon purpureus) (fragment)
#formal_name Ceratodon purpureus
13-Jan-1996 #sequence_revision 01-Mar-1996 #text_change
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#binding_site phytochromobilin (Cys) (covalent) #status
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Pred. No. 4.07e-196;
31; Mismatches 23;
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                                            #common_name potato
07-May-1993 #text_change
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FEATURE 76-588 333 ACCESSIONS REFERENCE RESULT ENTRY TITLE Š 뒪. Ş B CLASSIFICATION KEYWORDS GENETICS #introns B ş 망 CLASSIFICATION KEYWORDS GENETICS ORGANISM δ. SUMMARY SUMMARY FEATURE Query Match Best Local S Matches 14 Best Local Similarity 74.7%; Matches 142; Conservation 68-589 880-1139 #journal #title #authors Heyer, A.; Gatz, C.
#journal Plant Mol. Biol. (1992) 20:589-600
#title Isolation and characterization of a
potato type B phytochrome.
#cross-references MUID:93081720 #accession S62714 ##molecule_type DNA ##residues 1-1142 ##label LAG ##cross-references EMBL:U31284; NID:g1125698; PID:g1125699 #cross-references MUID:96191280 #authors #accession 136 287 ##molecule_type mRNA
##residues 1-1129 ##label HEY 187 407 347 ##status 76 ASRFLFKQNRVRMIVDCHATPVRVTQDESLMQPLCLVGSTLRAPHGCHAQYMANMGSIAS 346 LQLASQLAEK 196 LALAIVVKGKD--S-----LTLAVIINGNDEEAVGGGRNSMRLWGLVVGHHTSVRSIPFPLRYACEFLMQAFGLQLNME 406 LQLASQLSEK 416 AARFLFKQNRVRMICDCNATPVKVVQSEELKRPLCLVNSTLRAPHGCHTQYMANMGSVAS 146; 69.98; Similarity 69.58; 125/1; 298/3; 393/3; 468/3; 543/2; 621/3; 699/1; 856/2; 970/2; 1067/2 #superfamily phytochrome; phytochrome homology photoreceptor; phytochromobilin; transcription re Lagarias, D.M.; Wu, S.H.; Lagarias, J.C. plant Mol. Biol. (1995) 29:1127-1142 Atypical phytochrome gene structure in the Mesotaenium caldariorum. \$62714 #type complete
phytochrome lb - Mesotaenium caldariorum
#formal_name Mesotaenium caldariorum
19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change phyB
#superfamily phytochrome; phytochrome homology
photoreceptor; phytochromobilin; transcription predicted
#length 1129 #molecular-weight 125621 #checksum 8608 S28431 #length Conservative 15-Jan-1999 #domain phytochrome homology #label PHYT\
#domain signal transduction #status predi #domain phytochrome homology #label PHYT\
#binding_site phytochromobilin (Cys) (covalent) #status not compared with conceptual #binding_site phytochromobilin (Cys) (covalent) #status STD\ predicted #molecular-weight 125028 Score 1019; DB 2; Pred. No. 1.19e-193; 28; Mismatches 22; Score 1027; DB 2; Length 112; Pred. No. 1.92e-195; 23; Mismatches 16; Indels #status predicted #label ω translation Length 1129; Length 1142; cDNA-clone Indels 14; #checksum green coding regulation 9 regulation 785/1; Gaps for ω ω

Ş 밁 δÃ ACCESSIONS REFERENCE DATE RESULT ENTRY TITLE 8 밁 δõ В δÃ Š ğ 밁 δÃ 밁 Ş 망 밁 SUMMARY FEATURE KEYWORDS CLASSIFICATION REFERENCE ORGANISM Matches Query Match #journal #title 65-576 321 #journal FEBS Lett. (1993) 334:95-100
#title Mosses do express conventional,
phytochromes, Phytochrome of I
#cross-references MUID:94039823 #accession #authors #accession #description #submission #authors ##molecule_type mRNA ##residues 1-118,'M',120-1132 ##label KO2 ##cross-references EMBU:X75025 ##residues 1-1132 ##label KOL ##cross-references EMBL:X75025; NID:g402605; 383 172 121 323 380 CGFLMQVFGLQLNMEVESAAQLREK 404 121 320 260 EPYLGLHYPGTDIPQASRFLFMKNKVRIIADCSAPPVKVIQDPTLRQPVSLAGSTLRSPH 319 200 KLAAKAITRLQALPGGNIGLLCDTVVEEVRELTGYDRVMAYRFHEDEHGEVVAEIRRADL 259 167 263 ##status ##molecule_type mRNA 61 61 Match 69.7%; Local Similarity 67.8%; 1 KLAVRAISRLQSLPGGDIGALCDTVVEDVQRLTGYDRVMVYQFHEDDHGEVVSEIRRSDL EPYLGLHYPATDIPQAARFLFKQNRVRMICDCNATPVKVVQSEELKRPLCLVNSTLRAPH 120 PLRSACEFLMQVFGLQLNMEVELSSQLREK 412 GCHAQYMANMGSVASLVMAVIINDNSSEEGATAAGGILHKGRKLWGLVVCHHSSPRYVPF 382 GCHAQYMGNMGSIASLVMAVIINDNEEDSHGSVQRGRKLWGLVVCHHTSPRTVPFPLRSA 379 ø PLRYACEFLMQAFGLQLQMELQLASQLAEK 196 GCHTQYMANMGSVASLALAIVVKGK---D---SS---EPYLGLHYPATDIPQAARFLEMKNRVRIICDCSAPPVKVIQDPTMKHPISLAGSTLRGVH 322 CEFLMQAFGLQLQMELQLASQLAEK GCHTQYMANMGSVASLALAIVVKGK--DS--S----EPYLGLHYPATDIPQAARFLFKQNRVRMICDCNATPVKVVQSEELKRPLCLVNSTLRAPH 139; KOJUKISAOGIU, H.U.; Braun, B.; Schneider-Poetsch, H.J.A.W. submitted to the EMBL Data Library, September 1993 Evidence that mosses do express conventional B-type related phytochromes Phytochrome of Physcomitrella patens (Hedw.). \$37206 s3/206 #type complete phytochrome - moss (Physcomitrella patens) #formal_name Physcomitrella patens 13-Jan-1995 #sequence_revision 13-Jan-1995 17-Mar-1999 Kolukisaoglu, H.U.; Braun, B.; Martin, Schneider-Poetsch, H.A.W. #superfamily phytochrome; phytochrome homology
photoreceptor; phytochromobilin; transcription predicted
#length 1132 #molecular-weight 125230 #checksum S39070 S37206 S37206; S39070 Conservative #domain phytochrome homology #label PHYT\
#binding_site phytochromobilin (Cys) (cov preliminary Score 1016; DB 2; 1 Pred. No. 5.60e-193; 33; Mismatches 24; ss conventional, distantly B-type-related Phytochrome of Physcomitrella patens (He 196 Mismatches 24; PID:g402606 KLWGLVVGHHCSPRYVPF Length 1132; (Cys) (covalent) #status Indels ₩.F.; 9; regulation 7632 Gaps (Hedw.). 171 60 166 60

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#accession S12966
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##cross-references GB:S51224
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 CEFLMQAFGLQLQMELQLASQLAEK 196
                   CEFLMQVFGMQLNLHVELAAQLREK 403
                                                                   GCHTQYMANMGSVASLALAIVVKGKD--S--S----KLWGLVVGHHCSPRYVPFPLRYA 171
                                                                                                                                                                                                                                                                                       Similarity
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Thuemmler, F.; Dufner, M.; Kreisl, P.; Dittrich, P. submitted to the Protein Sequence Database, April 1992 Molecular cloning of a novel phytochrome gene of the moss Ceratodon purpureus which encodes a putative light
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              regulated protein kinase.
$20160
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Phytochrome in lower plants. Detection and partial sequence of a phytochrome gene in the moss Ceratodon purpureus using the polymerase chain reaction.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATP; phosphotransferase; photoreceptor; phytochromobilin; serine/threonine-specific protein kinase; transcription
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          #superfamily phytochrome / protein kinase; phytochrome homology; protein kinase homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          phy
679/1; 779
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                                                                                                                                                                                                                                                                     Score 986; DB 2; Le
Pred. No. 2.93e-186;
38; Mismatches 26;
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#authors
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#title
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                #accession S25401
##molecule_type mRNA
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             #authors
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##residues 1-1134 ##label HAN
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                                                                                                                                                                                                                                                                                                                                                      EPYLGLHYPATDIPQASRFLFMKNRVRMICDCSAPPVKITQDKELRQPISLAGSTLRAPH 322
                                                                                                                                                                                                                                                         GCHTQYMANMGSVASLALAIVVKGKD--SS----K---LWGLVVGHHCSPRYVPFP
                                                                                                                                                                                                                                                                                                                         LRSACEFLMQVFGLQLNMEAAVAAHVREK 410
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Similarity 68.9%;
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    spike moss
30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change
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phytochrome - Martens's sr
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Schneider-Poetsch, H.A.W.; Braun, B.
Schneider-Poetsch, (1991) 137:576-580
Proposal on the nature of phytochrome action
C-terminal sequences of phytochrome.
                              01-May-1998
S62721; S62717
S62720
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     predicted #length 1134 #molecular-weight 124706 #checksum
Hauser, B.A.;
Pratt, L.H.
                                                                            phytochrome B2 - tomato (fragment)
phytochrome B2 - tomato (fragment)
#formal_name Lycopersicon esculentum #common_name
19-Mar-1997 #sequence_revision 23-Aug-1997 #text_o
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    #domain phytochrome homology #label PHYT\
#binding_site phytochromobilin (Cys) (covalent) #status
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742 as Glu
                                               $62717
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Pred. No. 1.86e-182;
Pred. Total Press 25;
                 Cordonnier-Pratt,
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                  м.м.;
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                  Daniel-Vedele,
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Best Local Similarity 73.6%;
Matches 131; Conservative
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#title
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##molecule_type DNA
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#cross-references MUID:96191281

#accession $62717
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#accession S62716
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#description
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FICATION #superfamily phytochrome; phytochrome homology
DS photoreceptor; phytochromobilin
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##residues 1-1(
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                                        ##residues
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 EPYLGLHYPATDIPQAARFLFKQNRVRMICDCNATPVKVVQSEELKRPLCLVNSTLRAPH 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EPYIGLHYPATDIPQASRFLFKQNRVRMIVDCTAIPVRVIQDESLMQPLCLVGSTLRAPH 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 562720 #type fragment
phytochrome B1 - tomato (fragment)
#formal_name Lycopersioon esculentum #common_name tomato
27-Apr-1996 #sequence_revision 07-Feb-1997 #text_change
12-Feb-1999
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                                                                                                                                                     Pratt, L.H.
Plant Mol. Biol. (1995) 29:1143-1155
The phytochrome gene family in tomato
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Plant Mol. Biol. (1995) 29:1143-1155
  #superfamily phytochrome;
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Pratt, L.H.
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                                                                          nucleic acid sequence
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Pred. No. 4.09e-181;
22; Mismatches 17; Indels
phytochrome homology
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FEATURE 62-573 856-1111 318 ACCESSIONS REFERENCE KEYWORDS FEATURE 154 망 Ş 밁 Ş 밁 Ş RESULT ENTRY δÃ 밁 β 밁 ğ 멍 Š В CLASSIFICATION KEYWORDS GENETICS SUMMARY SUMMARY DATE ORGANISM TITLE Query Match Best Local S Matches 13 Query Match Best Local #authors Sharrock, R.A.; Quail, P.H.
#journal Genes Dev. (1989) 3:1745-1757
#title Novel phytochrome sequences in Arabidopsis thaliana:
structure, evolution, and differential expression (
plant regulatory photoreceptor family.
#cross-references MUID:90108670
#accession C33473 Matches 171 377 121 317 257 121 153 GCHAQYMANMGSIASLTLAVIINGNDEEAVGGGRNSMRLWGLVVGHHTSVRSIPFPLRY 211 ##residues 1-1111 ##label
##cross-references EMBL:X17343; ##molecule_type mRNA y Match 63.9%; Local Similarity 62.6%; hes 129; Conservative 61 61 93 33 Match 65.0%; Local Similarity 74.3%; ᆫ 14 KLAAKSISRLQALPSGNMLLLCDALVKEVSELTGYDRVMVYKFHEDGHGEVIAECCREDM 256 GCHAQYMSNMGSVASLVMSVTINGSDSDEMNRDLQTGRHLWGLVVCHHASPRFVPFPLRY 376 EPYLGLHYSATDIPQASRFLFMRNKVRMICDCSAVPVKVVQDKSLSQPISLSGSTLRAPH 316 EPYIGLHYPATDIPQASRFLFKQNRVRMVVDCHATPVRVTQDESLMQPLCLVGSTLRAPH 152 ACEFLTQVFGVQINKEAESAVLLKEK 402 EPYLGLHYPATDIPQAARFLFKQNRVRMICDCNATPVKVVQSEELKRPLCLVNSTLRAPH EPYLGLHYPATDIPQAARFLFKQNRVRMICDCNATPVKVVQSEELKRPLCLVNSTLRAPH 120 ACEFLMQAFGLQLQMELQLASQLAEK 196 GCHTQYMANMGSVASLALAIVVKG-----KD--SSK-LWGLVVGHHCSPRYVPFPLRY #domain phytochrome homology #label PHYT\
#domain signal transduction #label STD\
#binding_site phytochromobilin (Cys) (covalent) #status
predicted
#length 1111 #molecular-weight 123721 #checksum 3846 FKMUC #type complete
phytochrome C - Arabidopsis thaliana
#formal_name Arabidopsis thaliana #common_name mouse-ear 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 20-Feb-1998 photoreceptor; phytochromobilin #superfamily phytochrome; phytochrome homology
dimer; photoreceptor; phytochromobilin; transc: C33473; S07717 A33473 predicted #length 211 #checksum 274 Conservative regulation #binding_site phytochromobilin (Cys) (covalent) #status predicted Score 948; DB 2; Length 211 Pred. No. 9.21e-178; 23; Mismatches 14; Indels Score 931; DB 1; Length 1111; Pred. No. 5.76e-174; 36; Mismatches 31; Indels 10; SHA : NID:g16424; PID:g16425 Length 211; 9 Gaps Gaps of a 120 60 60 92 w •• Ψ

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##residues 1-1124 ##label SHA
##cross-references EMBL.M15265; NID:g167500; PID:g167501
##cross-references EMBL.M15265; NID:g167500; PID:g167500; 
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Search completed: Mon Sep 13 14:25:14 1999 Job time : 19 secs.
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Best Local Similarity 60.6%;
Matches 126; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  #authors Sharrock, R.A.; Lissemore, J.L.; Quail, P.H.
#journal Gene (1986) 47:287-295
#title Nucleotide and amino acid sequence of a Cucurbita phytochrome cDNA clone: identification of conserved features by comparison with Avena phytochrome.
#cross-references MUID:87163500
#accession S00099
                                                                                                                                                                                                                                                                                                                                                                                                                                                              169
                                                                                                                                                                                                                                     382 RYACEFLAQVFAIHVNKELELENQIIEK 409
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                                                                                                                                                    #domain phytochrome homology #label PHYT\
#domain signal transduction #label STD\
#binding_site phytochromobilin (Cys) (covalent) #status
predicted
#length 1124 #molecular-weight 125081 #checksum 3834
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FKFUZ #type complete phytochrome - zucchini
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 886; DB 1; Length 1124;
Pred. No. 6.21e-164;
37; Mismatches 33; Indels 12; Gaps
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(MT)

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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Tabular output not generated. Run on: Mon Sep 13 14:23:31 1999; MasPar time 7.13 Seconds 777.471 Million cell updates/sec

Description: Perfect Score: >US-09-272-809-9 (1-196) from US09272809.pep

1458

Sequence: 1 KLAVRAISRLQSLPGGDIGA......QAFGLQLQMELQLASQLAEK 196

Scoring table: PAM 150 Gap 11

Séarched: 77977 segs, 28268293 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: swiss-prot37 1:swissprot

Statistics: Mean 45.285; Variance 72.284; scale 0.626

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

1	Result No.
1431 11143 11143 11143 11070 10066 10058 11030 11030 11030 10106 996 996 997 1016 1016 1016 1016 1016 1016 1016 101	Score
100 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	,
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PHYE_PHANI PHYE_PHANI PHYE_PHANI PHYB_TOBAC PHY_PHYB_ARATH PHYB_ORYSA PHYB_SOLYBN PHYB_SOLYBN PHYT_CERPU PHYT_COBCC PHYT_TOBACC PHYA_CUCPE PHYA_CUCPE PHYA_CUCPE PHYA_COLTM PHYA_PEA	IĐ
PHYTOCHROME	Description
E. B. B. B. B. B. C. C. C. C. PROTEIN A.	
2.57e-301 3.10e-257 6.31e-236 3.71e-237 5.02e-235 4.99e-229 1.00e-227 6.06e-227 4.44e-224 7.11e-216 6.23e-214 6.23e-214 7.47e-212 2.85e-216 6.23e-192 3.82e-192 3.82e-192 3.82e-192 3.82e-193 5.69e-187 6.65e-185	Pred. No.

45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24
88	89	89	90	91	91	96	101	100	102	104	105	105	552	831	836	837	845	845	860	865	864
6.0	6.1	6.1	6.2	6.2	6.2	б. б	6.9	6.9	7.0	7.1	7.2	7.2	37.9	57.0	57.3	57.4	58.0	58.0	59.0	59.3	59.3
810	502	242	485	379	349	360	874	386	255	407	715	422	748	1131	1128	1128	1128	494	1131	1129	1124
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YP07_YEAST	SKS1_YEAST	RSTA_ECOLI	SAHH_MESCR	HUPD_AZOCH	IHBB_PIG	LEU3_PSEAE	DP3A_MYCGE	CYB_HANWI	IHBB_MOUSE	IHBB_HUMAN	Y07J_MYCTU	YURO_BACSU	Y473_SYNY3	PHYA_MAIZE	PHYA_ORYSA	PHY3_AVESA	PHY4_AVESA	PHY5_AVESA	PHYA_SOYBN	PHYA_PETCR	PHYA_LATSA
HYPOTHETICAL 89.8 KD P	SERINE/THREONINE-PROTE	TRANSCRIPTIONAL REGULA	ADENOSYLHOMOCYSTEINASE	HYDROGENASE EXPRESSION	INHIBIN BETA B CHAIN P	3-ISOPROPYLMALATE DEHY	DNA POLYMERASE III, AL	CYTOCHROME B (EC 1.10.	INHIBIN BETA B CHAIN P	BETA B CHAIN	TICAL		84.2	PHYTOCHROME A.		PHYTOCHROME A TYPE 3 (A	A TYPE	Α.		
2.11e+00	1.52e+00	1.52e+00	1. IUe+00	7.85e-UL	7.85e-01	1.42e-U1	2.39e-02	3.43e-02	1.66e-02	7.98e-03	5.5Le-03	5.51e-03	4.55e-105	3.96e-1/6	2.03e-1//	1.12e-1//	9./Ue-180	9./00-180	1.30e-183	6.65e-185	1.21e-184

ALIGNMENTS

DR DR C	88888888	888888888	CC CC RT R R R R R R R R R R R R R R R R	RESULT P ACC P DT OCC C E E C C C C C C C C C C C C C C C
MBL; X76610; G452817; ROSITE; PS00245; PHYT ROSITE; PS50046; PHYT FAM; PF00360; phytoch	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).	PFR INDUCES AN ARRAY OF MORPHOSENIC RESPONSES, WHEREAS RECONVERSION OF PFR TO PR CANCELS THE INDUCTION OF THOSE RESPONSES, PFR CONTROLS THE EXPRESSION OF A NUMBER OF NUCLEAR GENES INCLUDING THOSE ENCODING THE SMALL SUBUNIT OF RIBULOSE- BISPHOSPHATE CARBOXYLASE, CHLOROPHYLL A/B BINDING PROTEIN, PROTOCHLOROPHYLLIDE REDUCTASE, RNA, ETC. IT ALSO CONTROLS THE EXPRESSION OF ITS OWN GENE(S) IN A NEGATIVE FEEDBACK FASHION!- SUBUNIT: HOMODIMER!- PTM: CONTAINS ONE COVALENTLY LINKED TETRAPYRROLE CHROMOPHORE.	SEQUENCE FROM N.A. SEQUENCE FROM N.A. SEQUENCE FROM N.A. STRAIN-CV. LANDSBERG ERECTA; CLACK T., MANHEWS S., SHARROCK R.A.; CLACK T., MANHEWS S., SHARROCK R.A.; The phytochrome apoprotein family in Arabidopsis is encoded by five "The phytochrome apoprotein family and PHYE."; genes: the sequences and expression of PHYD and PHYE."; PLANT MOL. BIOL. 25:413-427(1994). PLA	PRT; 1112 AA. PHYE_ARATH STANDARD; PRT; 1112 AA. P42498; 01-NOV-1995 (REL. 32, CREATED) 01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE) 01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE) PHYTOCHROME E. PHYE. P

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Matches
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01-0CT-1996
01-0CT-1996
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P55004;
                                                                                                                                                                                                                                                                                                                                                                                                                ZHENG C.C., O'NEILL S.D.;
SUBMITTED (JAN-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
SUBMITTED (JAN-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.

-!- FUNCTION: REGULATORY PHOTORECEPTOR WHICH EXISTS IN TWO FORMS THAT
ARE REVERSIBLY INTERCONVERTIBLE BY LIGHT: THE PR FORM THAT ABSORBS
WAXIMALLY IN THE FED REGION OF THE SPECTROM AND THE PRE FORM THAT
ABSORBS MAXIMALLY IN THE FAR-YED REGION. PHOTOCONVERSION OF PR IN
ABSORBS MAXIMALLY IN THE FAR-YED REGION. PHOTOCONVERSION OF PR IN
ABSORBS MAXIMALLY IN THE FAR-YED REGION. PHOTOCONVERSION OF PR IN
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ABSORBS MAXIMALLY IN THE FAR-YED REGION. PHOTOCONVERSION OF PR IN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PHARBITIS NIL (VIOLET) (JAPANESE MORNING GLORY).
EUKARYOTA; VIRIDIPLANTAE; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA;
EUPHYLLOPHYTES; SPERMATOPHYTA; MAGNOLIOPHYTA; EUDICOTYLEDONS;
ASTERIDAE; SOLANANAE; SOLANALES; CONVOLVULACEAE; IPOMOEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PFAM; PF00989; PAS; MENDEL; 7190; ARAth
                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE-SEEDLING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A
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                                                                                                                                     entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
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Local Similarity 100.0%;
les 196; Conservative
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                                                                                                                                                                                                                                                                            SUBUNIT:
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(REL.
                                                                                                                                                                                                                                                                                              HOMODIMER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COTYLEDON;
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34, LAST SEQUENCE UPDATE)
34, LAST ANNOTATION UPDATE)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 1458; DB 1;
Pred. No. 0.00e+00;
0; Mismatches 0
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Best Local (
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                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NICOTIANA TABAGUM (COMMON TOBACCO).
EUKARYOTA; VIRIDIPLANTAE; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA;
EUFHYLLOPHYTES; SPERWATOPHYTA; MAGNOLIOPHYTA; EUDICOTYLEDONS;
ASTERIDAE; SOLANANAE; SOLANALES; SOLANACEAE; NICOTIANA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PHYB
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                                                                                                                                                                                                                                                                                                                                                                            PLANT CELL 4:241-251(1992)
-1- FUNCTION: REGULATORY P
                                                                                                                                                                                                                                                                                                                                                                                                                                      LOPEZ-JUEZ E., NAGATANI A.,
KENDRICK R.E., FURUYA M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KERN R., GASCH A., DI
SUBMITTED (XXX-1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PHYTOCHROME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-FEB-1994
01-NOV-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                           phytochrome.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 457-1132 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KERN R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                          "The cucumber long hypocotyl mutant lacks a light-stable PHYB-like
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                                                                                                                                                                                                       FUNCTION: REGULATORY PHOTORECEPTOR WHICH EXISTS IN TWO FORMS THAT ARE REVERSIBLY INTERCONVERTIBLE BY LIGHT: THE PR FORM THAT ABSORBS MAXIMALLY IN THE RED REGION OF THE SPECTRUM AND THE PER FORM THAT ABSORBS MAXIMALLY IN THE FAR-RED REGION. PHOTOCONVERSION OF PR IN PRINCIPLE OF MARRAY OF MORPHOGENIC RESPONSES, WHEREAS RECONVERSION OF PR TO PR CANCELS THE INDUCTION OF THOSE RESPONSES. PER CONTROLS THE EXPRESSION OF A NUMBER OF NUCLEAR GENES INCLUDING THOSE ENCODING THE SMALL SUBBNIT OF RIBULOSE-BISPHOSPHATE CARBOXYLASE, CHLOROPHYLL AVB BINDING PROTEIN, PROTOCHLOROPHYLLIDE REDUCTASE, RRNA, ETC. IT ALSO CONTROLS THE EXPRESSION OF IT ALSO CONTROLS THE EXPRESSION OF IT ALSO CONTROLS.
                                                                                                                                                                              PTM: CONTAINS
                                                                                                                                                                                              SUBUNIT: HOMODIMER.
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 L10114; G295346; -.
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larity 87.2%;
Conservative
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                                                                                                                                                                              ONE COVALENTLY LINKED TETRAPYRROLE CHROMOPHORE
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28, LAST SEQUENCE UPDATE)
32, LAST ANNOTATION UPDATE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         M., KAY S.A., CHUA N.H.;
EMBL/GENBANK/DDBJ DATA BANKS
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OCONVERSION OF PR IN
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Best Local
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PFAM; PF00512; signal; 1.
PFAM; PF00989; PAS; 2.
MENDEL; 1321; NICta; PhyB; 1.
TRANSCRIPTION REGULATION; PHOTORECEPTOR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PHY_PINSY
Q41046;
01-NOV-1997
01-NOV-1997
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between
the Euro
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                                                                                                                                                                                                                                                                                                                                                                               PINUS SYLVESTRIS (SCOTS PINE).
EUKARYOTA; VIRIDIPLANTAE; STREPTOPHYTA; EMBRYGEUPHYLLOPHYTES; SPERMATOPHYTA; CONIFEROPSIDA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BINDING
                                     use by non-profit institutions as long modified and this statement is not removed. entities requires a license agreement (See or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PHYTOCHROME
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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                                                                                                                                                                                                                               RECONVERSION OF PFR TO PR CANCELS THE INDUCTION OF THOSE RESPONSES. PFR CONTROLS THE EXPRESSION OF A NUMBER OF NUCLEAR GENES INCLUDING THOSE ENCOURING THE SMALL SUBUNIT OF RIBULOSE-BISPHOSPHATE CARBOXYLASE, CHLOROPHYLL A/B BINDING PROTEIN, PROTOCHLOROPHYLLIDE REDUCTASE, RNA, ETC. IT ALSO CONTROLS THE EXPRESSION OF ITS OWN GENE(S) IN A NEGATIVE FEEDBACK FASHISHED THE EXPRESSION OF ITS OWN GENE(S) IN A NEGATIVE FEEDBACK FASHISHED THE EXPRESSION OF ITS OWN GENE(S) IN A NEGATIVE FEEDBACK FASHISHED THE EXPRESSION OF ITS OWN GENE(S) IN A NEGATIVE FEEDBACK FASHISHED THE EXPRESSION OF ITS OWN GENE(S) IN A NEGATIVE FEEDBACK FASHISHED THE EXPRESSION OF ITS OWN GENE(S) IN A NEGATIVE FEEDBACK FASHISHED THE EXPRESSION OF ITS OWN GENE(S) IN A NEGATIVE FEEDBACK FASHISHED THE EXPRESSION OF ITS OWN GENE(S) IN A NEGATIVE FEEDBACK FASHISHED THE EXPRESSION OF ITS OWN GENE(S) IN A NEGATIVE FEEDBACK FASHISHED THE EXPRESSION OF ITS OWN GENE(S) IN A NEGATIVE FEEDBACK FASHISHED THE EXPRESSION OF ITS OWN GENE(S) IN A NEGATIVE FEEDBACK FASHISHED THE EXPRESSION OF ITS OWN GENE(S) IN A NEGATIVE FEEDBACK FASHISHED THE EXPRESSION OF ITS OWN GENE(S) IN A NEGATIVE FEEDBACK FASHISHED THE EXPRESSION OF ITS OWN GENE(S) IN A NEGATIVE FEEDBACK FASHISHED THE EXPRESSION OF ITS OWN GENE(S) IN A NEGATIVE FEEDBACK FASHISHED THE EXPRESSION OF ITS OWN GENE(S) IN A NEGATIVE FEEDBACK FASHISHED THE SAME FA
                                                                                                        s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way
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157; Conse
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77.0%;
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LAST ANNOTATION UPDATE)
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L -> S (IN REF. 2).

L -> LQ (IN REF. 2).

MW; 6CD35D63 CRC32;
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25; 1
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Pred. No. 3.10e-257;
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                                                              noved. Usage by and for (See http://www.isb-sib
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBRYOPHYTA; TRACHEOPHYTA; PSIDA; CONIFERALES; PINACEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PHYTOCHROME; CHROMOPHORE;
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                                                                                    Usage
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P14713;
01-APR-1990
01-APR-1990
01-NOV-1995
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SEQUENCE
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PROSITE; PS50046; PHYTOCHROD
PROM; PP00360; Phytochrome;
PFAM; PF00512; Signal; 1.
PFAM; PF00989; PAS; 2.
PFAM; PF00989; PAS; 2.
                                                                                                                                                                                 REED J.W., NAGPAL P., POOLE D.S., FURUYA M., CHORY J.;
"Mutations in the gene for the red/far-red light receptor phyto
B alter cell elongation and physiological responses throughout
Arabidopsis development.";
PLANT CELL 5:147-157(1993).
-I- FUNCTION: RECHTARCOL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TRANSCRIPTION REGULATION; PHOTORECEPTOR; PHYTOCHROME; CH
BINDING 332 332 CHROMOPHORE (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=CV.
MEDLINE; 9
                                                                                                                                                                                                                                                                                                                                                                     MEDLINE; 90108670.
SHARROCK R.A., QUALL P.H.;
"Novel phytochrome sequences in Arabidopsis thaliana: structure, evolution, and differential expression of a plant regulatory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).
EUKARYOTA; VIRIDIPLANTAB; STROPHYTA; EMBRYG
EUKARYOTA; PERMATOPHYTA, MAGNOLIOPHYTA;
EUPHYTLOPHYTES; SPERMATOPHYTA, MAGNOLIOPHYTA;
CAPPARALES; BRASSICACEAE; ARABIDOPSIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PHYTOCHROME
                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. STRAIN-CV. LANDSBE
                                                                                                                                                                                                                                                                                                                                           photoreceptor family.";
GENES DEV. 3:1745-1757(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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           FUNCTION: REGULATORY PHOTORECEPTOR WHICH EXISTS IN TWO FORMS THAT ARE REVERSIBLY INTERCONVERTIBLE BY LIGHT: THE PR FORM THAT ABSORBS MAXIMALLY IN THE RED REGION OF THE SPECTRUM AND THE PFR FORM THAT ABSORBS MAXIMALLY IN THE FAR-RED REGION, PHOTOCONVERSION OF PR INDUCES AN ARRAY OF MORPHOGENIC RESPONSES, WHEREAS RECONVERSION OF PFR TO PR CANCELS THE INDUCTION OF THOSE RESPONSES, PPR CONTROLS THE EXPRESSION OF A NUMBER OF NUCLEAR GENES INCLUDING THOSE ENCODING THE SMALL SUBUNIT OF RIBULOSE-BISPHOSPHATE CARBOXYLASE, CHLOROPHYLL A/B BINDING PROTEIN, PROTOCHLOROPHYLLIDE REDUCTASE, RRNA, ETC. IT ALSO CONTROLS THE EXPRESSION OF ITS OWN GENE(S) IN A NEGATIVE FEEDBACK FASHION. SUBUNIT: HOMODIMER.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14, CREATED)
14, LAST SEQUENCE UPDATE)
32, LAST ANNOTATION UPDATE
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78.5%;
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   COVALENTLY LINKED
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Pred.
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No. 6.31e-256;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBRYOPHYTA; TRACHEOPHYTA;
PHYTA; EUDICOTYLEDONS; ROSIDAE;
   TETRAPYRROLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 1131;
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    CHROMOPHORE
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a collaboration

EMBL; X17342;

G16423; -

-; NOT_ANNOTATED_CDS.

PIR; S07718; FKMUB.

PIR; JQ2141; JQ2141.

PROSITE; PS00245; PHYTOCHROME_1; 1.

PROSITE; PS50046; PHYTOCHROME_2; 1.

PFAM; PF00360; phytochrome; 1. PFAM; PF00512; signal; 1. PFAM; PF00989; PAS; 2.

MENDEL; 1310; ARAth; PhyB;1.
TRANSCRIPTION REGULATION; PHOTORECEPTOR; PHYTOCHROME; CHROMOPHORE;

SEQUENCE BINDING

MULTIGENE

FAMILY. 357 3 1172 AA;

25 357

GLY/SER-RICH. CHROMOPHORE.

129331

MW;

2FC0BA87 CRC32;

Length 1172;

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60

120

169

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RESULTION OF THE PROPERTY OF T
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Best Local S
Matches 15
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01-MAY-1992
01-NOV-1995
phyb is evolution.

Ice seedling shoets.",

OL. GEN. GENET. 225:305-313(1991).

OL. GEN. GENET. 225:305-313(1991).

OL. GEN. GENET. 225:305-313(1991).

OL. GEN. GENET. 225:305-313(1991).

IF FUNCTION: REGULATORY PHOTORECEPTOR WHICH EXISTS IN TWO FORMS THAT ABSORBS MAXIMALLY INTERCONVERTIBLE BY LIGHT: THE PR FORM THAT ABSORBS MAXIMALLY IN THE FAR-RED REGION. PHOTOCONVERSION OF PR IN ABSORBS MAXIMALLY IN THE FAR-RED REGION. PHOTOCONVERSION OF PR IN PER INDUCES AN ARRAY OF MORPHOGENIC RESPONSES, WHEREAS RECONVERSION OF PR TO PR CANCELS THE INDUCTION OF THOSE RECONVERSION OF PR TO PR CANCELS THE INDUCTION OF THOSE RECONVERSION OF PR TO PR CANCELS THE INDUCTION OF NUCLEAR
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ORYZA SATIVA (GICE).

EUKARYOTA; VIRIDIPLANTAE; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA; EUPHYLLOPHYTES; SPERMATOPHYTA; MAGNOLIOPHYTA; LILIOPSIDA; POALES;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PHYB_
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PHYTOCHROME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-CV. INDICA-IR36; MEDLINE; 91172131.
                                                                                                                                                                                                                                                                                                                                                                                                                                   DEHESH K., TEPPERMAN J., CHRISTENSEN A.H., QUAIL P.H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POACEAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               236 KLAVRAISQLQALPGGDIKLLCDTVVESVRDLTGYDRVMYYKFHEDEHGEVVAESKRDDL
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(REL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22, CREATED)
22, LAST SEQUENCE UPDATE)
32, LAST ANNOTATION UPDATE)
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73.98;
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Pred. No. 3.71e-238;
25; Mismatches 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
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Best Local
                                                                                                                                                                                                                                                                                        PHYB.
GLYCINE MAX (SOYBEAN).
EURARYOTA, VIRIDIPLANTAE; S'
EUPHYLLOPHYTES; SPERMATOPHY
FABALES; FABACEAE; PAPILION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P42499;
01-NOV-1995
01-NOV-1995
15-DEC-1998
                       SEQUENCE FROM N.A.

STRAIJ-CV. PALDAL; TISSUE-ETIOLATED LEAF;
HAHN T.R., WOO T.W., SEO H.S., CHOI Y.D.;
SUBMITTED (XXX-1994) TO EMBL/GENBANK/DDBJ DATA BANKS.

-!- FUNCTION: REGULATORY PHOTORECEPTOR WHICH EXISTS IN TWO FORMS THAT ARE REVERSIBLY INTERCONVERTIBLE BY LIGHT: THE PR FORM THAT ABSORBS MAXIMALLY IN THE RED REGION OF THE SPECTRUM AND THE PFR FORM THAT ABSORBS MAXIMALLY IN THE FAR-RED REGION. PHOTOCONVERSION OF PR IN PER INDUCES AN ARRAY OF MORPHOGENIC RESPONSES, WHEREAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation—the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PFAM; PF00360; phytochrome; PFAM; PF00512; signal; 1. PFAM; PF00989; PAS; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PHYTOCHROME
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; X57563;
PIR; S14065; S
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PTM: CONTAINS ONE COVALENTLY LINKED TETRAPYRROLE CHROMOPHORE
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BISPHOSPHATE CARBOXYLASE, CHLOROPHYLL A/B BINDING PROTEIN,
PROTCCHLOROPHYLLIDE REDUCTASE, RRNA, ETC. IT ALSO CONTROLS
THE EXPRESSION OF ITS OWN GENE(S) IN A NEGATIVE FEEDBACK FASHION.
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11 Similarity 72.78;
152; Conservation
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1171 AA;
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37,
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364 CHROMOPHORE (BY SIMILARITY).
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     PFR TO PR
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LAST ANNOTATION UPDATE)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 1066; DB 1;
Pred. No. 4.11e-237;
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RESPONSES. PFR CONTROLS THE EXPRESSION OF A NUMBER OF NUCLIGENES INCLUDING THOSE ENCODING THE SMALL SUBUNIT OF RIBULOS BISPHOSPHATE CARBOXYLASE, CHLOROPHYLL A/B BINDING PROTEIN, PROTOCHLOROPHYLLIDE REDUCTASE, RRNA, ETC. IT ALSO CONTROLS THE EXPRESSION OF ITS OWN GENE(S) IN A NEGATIVE FEEDBACK FURNAL STREET OF THE EXPRESSION OF THE OWN GENE(S) IN A NEGATIVE FEEDBACK FURNAL STREET OWN GENE (S) IN A NEGATIVE FURNAL STREET OWN GENE (S) IN A NEGATIVE FURNAL STREET OWN GENE (S) IN A NEGATIVE FURNAL STREET OWN GENE GENE GOVER OWN GENE GOVER OWN GENE GOVER OWN GENE GOVER OWN GENE GOVER GOVER OWN GENE GOVER

SUBUNIT: HOMODIMER.
PTM: CONTAINS ONE COVALENTLY LINKED TETRAPYRROLE CHROMOPHORE.

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P42496;
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PROSITE; PS00245; PHYTOCHROME_2; 1.

PROSITE; PS50046; PHYTOCHROME_2; 1.

PFAM; PF00360; Phytochrome; 2.

PFAM; PF00512; signal; 1.

PFAM; PF00989; PAS; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                     MENDEL; 8366; GLYma; PhyB; 1 TRANSCRIPTION REGULATION;
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                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                         ADIANTUM CAPILLUS-VENERIS (FERN).
EUKARYOTA; VIRIDIPLANTAE; STREPTOPHYTA; EMBRYOPHYTA;
EUPHYLLOPHYTES; FILICOPHYTA; FILICOPSIDA; FILICALES;
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32,
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27; Mismatc
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                                                                                                                                                                                                                                                                                                                                                              Mismatches 19;
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                                                                                                                                                             UPDATE)
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                                                                                                                             TRACHEOPHYTA;
ADIANTACEAE;
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01-NOV-1995
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PHYTOCHROME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; D13519; D1003241; --
PROSITE; PS00245; PHYTOCHROME_1;
PROSITE; PS0046; PHYTOCHROME_2;
PFAM; PF00360; phytochrome; 1.
PFAM; PF00512; signal; 1.
PFAM; PF00989; PAS; 2.
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                STRAIN-CV. LANDSBERG ERECTA;

STRAIN-CV. LANDSBERG ERECTA;

STRAIN-CV. LANDSBERG ERECTA;

CLACK T., MATHEWS S., SHARROCK R.A.;

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                                                                                                                                                                                                                                                                                ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).
EURARYOTA; VIRIDIPLANTAE; STREPTOPHYTA; EMBRYC
EUPHYLLOPHYTES; SPERMATOPHYTA; MAGNOLIOPHYTA;
                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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sen the Swiss Institute of Bioinformatics and the E
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1117 AA;
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ANNOTATION UPDATE)
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SUBUNIT: HOMODIMER.
PTM: CONTAINS ONE COVALENTLY LINKED TETRAPYRROLE CHROMOPHORE.

GENES INCLUDING THOSE ENCODING THE SMALL SUBUNIT OF RIBULOSE-BISPHOSPHATE ARBOXYLASE, CHLOROPHYLL A/B BINDING PROTEIN, PROTOCHLOROPHYLLIDE REDUCTASE, RRNA, ETC. IT ALSO CONTROLS THE EXPRESSION OF ITS OWN GENE(S) IN A NEGATIVE FEEDBACK FASHION.

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Best Local
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Q39557;
Q1-NOV-1997
Q1-NOV-1997
Q1-NOV-1998
SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

LAMPARTER T., MITTMANN F.;

"CERPU; PHY0; 2. a 'normal' phytochrome in Ceratodon.";

"CERPU; PHY0; 2. a 'normal' phytochrome in Ceratodon.";

"LAMPARTER T., a 'normal' phytochrome in Ceratodon.";

"I' FUNCTION: REGISTER PGR96-067.

-i- FUNCTION: REGULATORY PHOTORECEPTOR WHICH EXISTS IN TWO FORMS THAT ARE REVERSIBLY INTERCONVERTIBLE BY LIGHT: THE PR FORM THAT ABSORBS MAXIMALLY IN THE FEGION OF THE SPECTRUM AND THE PER FORM THAT ABSORBS MAXIMALLY IN THE FAR-RED REGION. PHOTOCONVERSION OF PR IN PER INDUCES AN ARRAY OF MORPHOGENIC RESPONSES, WHEREAS PER INDUCES AN ARRAY OF MORPHOGENIC RESPONSES, WHEREAS RESPONSES. PER CONTROLS THE EXPRESSION OF A NUMBER OF NUCLEAR GENES INCLUDING THOSE ENCODING THE SMALL SUBUNIT OF RIBULOSE-BISPHOSPHATE CARBOXYLASE, CHLOROPHYLL A/B BINDING PROTEIN,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CERATODON PURPUREUS (MOSS).
EUKARYOTA; VIRIDIPLANTAE; STREPTOPHYTA; EMBRYOPHYTA; BRYOPSIDA;
BRYIDAE; DICRANALES; DITRICHACEAE; CERATODON.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PFAM; PF00360; phytochrome; 1.
PFAM; PF00512; signal; 1.
PFAM; PF00989; PAS; 2.
MENDEL; 7189; ARAth; PhyD; 1.
TRANSCRIPTION REGULATION; PHOTORECEPTOR; PHYTOCHROME; CHROMOPHORE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; X76609; G452814; -.
PROSITE; PS00245; PHYTOCHROME_1;
PROSITE; PS50046; PHYTOCHROME_2;
PFAM; PF00360; phytochrome; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MULTIGENE FAMILY.
BINDING 360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GCHTQYMANMGSVASLALAIVVKGK--D----S---S-KLWGLVVGHHCSPRYVPFPL
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Similarity 71.2%;
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(REL.
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35, LAST SEQUENCE SEQUENCE
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ANNOTATION
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Pred. No. 3.02e-228;
30; Mismatches 18;
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WW; 6BC8A3F1 CRC32;
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Best Local S
Matches 14
                      Type B phytochrome.";

PLANT MOL. BIOL. 20:589-600(1992).

FI FUNCTION: REGULATORY PHOTORECEPTOR WHICH EXISTS IN TWO FORMS THAT ARE REVERSIBLY INTERCONVERTIBLE BY LIGHT: THE PR FORM THAT ABSORBS MAXIMALLY IN THE RED REGION OF THE SPECTRUM AND THE PER FORM THAT ABSORBS MAXIMALLY IN THE FAR-RED REGION. PHOTOCONVERSION OF PR IN PER INDUCES AN ARRAY OF MORPHOGENIC RESPONSES, WHEREAS RECONVERSION OF PER TO PR CANCELS THE INDUCTION OF THOSE RECONVERSION OF PER TO PR CANCELS THE INDUCTION OF THOSE
                                                                                                                                                                                                                                                                                                                                      PHYB_SOLTU
P34094;
01-FEB-1994
01-FEB-1994
01-OCT-1996
                                                                                                                                                                                                                                                               SOLANUM TUBEROSUM (POTATO).
EUKARYOTA; VIRIDIPLANTAE; STREI
EUPHYLLOPHYTES; SPERMATOPHYTA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PFAM; PF00360; phytochrome; PFAM; PF00512; signal; 1. PFAM; PF00989; PAS; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                   HEYER A., GATZ C.;
"Isolation and characterization
                                                                                                                                                                                                 SEQUENCE FROM N.A. MEDLINE; 93081720.
                                                                                                                                                                                                                                                                                                           PHYB
                                                                                                                                                                                                                                                                                                                           PHYTOCHROME
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BINDING 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TRANSCRIPTION REGULATION; PHOTORECEPTOR; PHYTOCHROME; CHROMOPHORE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; U56698; G1314837;
                                                                                                                                                                                                                                                ASTERIDAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               172
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PTM: CONTAINS ONE COVALENTLY LINKED TETRAPYRROLE CHROMOPHORE.
RESPONSES. PER CONTROLS THE EXPRESSION OF A NUMBER OF NUCLEAR GENES INCLUDING THOSE ENCODING THE SMALL SUBUNIT OF RIBULOSE-BISPHOSPHATE CARBOXYLASE, CHLOROPHYLL A/B BINDING PROTEIN,
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1121 AA;
                                                                                                                                                                                                                                                SOLANANAE;
                                                                                                                                                                                                                                                                                                                                        (REL.
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larity 69.3%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
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28, LAST SEQUENCE UPDATE)
34, LAST ANNOTATION UPDATE)
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                                                                                                                                                                                                                                                SOLANALES; SOLANACEAE;
                                                                                                                                                                                                                                                            STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA; STACHEOPHYTA; HYTA; MAGNOLIOPHYTA; EUDICOTYLEDONS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 1030; DB 1;
Pred. No. 1.00e-227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         31; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             402
                                                                                                                                                                   of a cDNA-clone coding for
                                                                                                                                                                                                                                                                                                                                                                                                    1129
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There are no restrictions on ong as its content is in no
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                                                                                                                                                                                                                                               SOLANUM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 1121;
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-!- PTM: CONTAINS ONE COVALENTLY LINKED TETRAPYRROLE CHROMOPHORE

PROTOCHLOROPHYLLIDE REDUCTASE, RRNA, ETC. IT ALSO CONTROLS THE EXPRESSION OF ITS OWN GENE(S) IN A NEGATIVE FEEDBACK FI SUBUNIT: HOMODIMER.

FEEDBACK FASHION

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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JUN-1994 (REL. : 01-JUN-1994 (REL. : 01-NOV-1995 (REL. : PHYTOCHROME 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; S51538; G261209; -.
PIR; S28431; S28431; PROSITE; PS00245; PHYTOCHROME_1;
PROSITE; PS50046; PHYTOCHROME_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PHY1_PHYPA
P36505;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MENDEL;
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                                                                                                                                                                                                                                                                                     "Mosses do express conventional, distantly in phytochromes. Phytochrome of Physcomitrella FEBS LETT. 334,95-100(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PHYSCOMITRELLA PATENS (MOSS).
EUKARYOTA; VIRIDIPLANTAE; STR
                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. MEDLINE; 94039823.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        227
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                                                                                                                                                                                                                                                                                                                                                                                                      KOLUKISAOGLU H.U.,
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FUNCTION: REGULATORY PHOTORECEPTOR WHICH EXISTS IN TWO FORMS THAT ARE REVERSIBLY INVERCONVERTIBLE BY LIGHT: THE PR FORM THAT ABSORBS MAXIMALLY IN THE RED REGION OF THE SPECTRUM AND THE PER FORM THAT ABSORBS MAXIMALLY IN THE FAR-RED REGION. PHOTOCONVERSION OF PR IN PER INDUCES AN ARRAY OF MORPHOGENIC RESPONSES, WHEREAS RECONVERSION OF PR TO PR CANCELS THE INDUCTION OF THOSE RESPONSES. PER CONTROLS THE EXPRESSION OF A NUMBER OF NUCLEAR GENES INCLUDING THOSE ENCODING THE SMALL SUBUNIT OF RIBULOSE-
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. 29, LAST SEQUENCE. 32, LAST ANNOTES.
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74.78;
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LAST ANNOTATION UPDAT
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Pred. No. 6.06e-227;
23; Mismatches 16;
                                                                                                                                                                                                                                                                                                                                                                MARTIN W.F., SCHNEIDER-POETSCH H.A.W.; nal, distantly B-type-related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CHROMOPHORE
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PROSITE; PS00245; PHYTOCHROME_2; 1

PROSITE; PS50046; PHYTOCHROME_2; 1

PFAM; PF00360; phytochrome; 1.

PFAM; PF00989; PAS; 2.

PFAM; PF00989; PAS; 2.

PFAM; PF00989; PAS; 2.
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Q40762;
01-NOV-1997
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BINDING 321 321 CHROMOPHORE (BY SIMILARITY).
                                                                                                                     SEQUENCE FROM N.A.

CLAPHAM D.H., LARSSON C.T., QAMARUDDIN M.;

SUBMITTED (JUL-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.

SUBMITTED (JUL-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.

-I- FUNCTION: REGULATORY PHOTORECEPTOR WHICH EXISTS IN TWO FORMS THAT ARE REVERSIBLY INTERCONVERTIBLE BY LIGHT: THE PR FORM THAT ABSORBS ANAXIMALLY IN THE FAR RED REGION. PHOTOCONVERSION OF PR IN PRINTED REGION. PHOTOCONVERSION OF PRINTED REGION. PRINTED REGI
                                                                                                                                                                                                                                                                                                                                                                                                                     PICEA ABIES (NORWAY SPRUCE) (PICEA EXCELSA).
EUKARYOTA; VIRIDIPLANTAE; STREPTOPHYTA; EMBR
EUPHYLLOPHYTES; SPERMATOPHYTA; CONIFEROPSIDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BISPHOSPHATE CARBOXYLASE, CHLOROPHYLL A/B BINDING PROTEIN, PROTOCHLOROPHYLLIDE REDUCTASE, RRNA, ETC. IT ALSO CONTROLS THE EXPRESSION OF ITS OWN GENE(S) IN A NEGATIVE FEEDBACK F.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUBUNIT: HOMODIMER.
GENES INCLUDING THOSE ENCODING THE SMALL SUBUNIT OF RIBULOSE: BISPHOSPHATE CARBOXYLASE, CHLOROPHYLL A/B BINDING PROTEIN, PROTOCHLOROPHYLLIDE REDUCTASE, RRNA, ETC. IT ALSO CONTROLS THE EXPRESSION OF ITS OWN GENE(S) IN A NEGATIVE FEEDBACK FASH SUBUNIT: HOMODIMER (BY SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CEFLMQAFGLQLQMELQLASQLAEK
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(REL.
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LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDAT
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pred. No. 4.44e-224;
33; Mismatches 24;
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PSIDA; CONIFERALES; PINACEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -KLWGLVVGHHCSPRYVPFPLRYA
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                                   FEEDBACK FASHION
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Best 1
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                                                                                                                                                                                                                                                                                                                                              "Molecular cloning of a novel phytochrome gene of i purpureus which encodes a putative light-regulated PLANT MOL. BIOL. 20:1003-1017(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CERATODON PURPUREUS (MOSS).
EUKARYOTA; VIRIDIPLANTAE; STREPTOPHYTA; EMBRYOPHYTA; BRYOPSIDA;
BRYIDAE; DICRANALES; DITRICHACEAE; CERATODON.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P25848; P93100;

U1-MAY 1992 (REL. 22, CREATED)

15-JUL-1998 (REL. 36, LAST SEQUENCE UPDATE)

15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)

PHYTOCHROME / PROTEIN KINASE (EC 2.7.1.-).

PHY1 OR PHY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         between the Swiss Institute of Bioinformatics and the E the European Bioinformatics Institute. There are no rest use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an entitles requires a license agreement (See http://www.isb-or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TRANSCRIPTION REGULATION; PHOTORECEPTOR; PHYTOCHROME; CHROMOPHORE.
BINDING 336 336 CHROMOPHORE (BY SIMILARITY).
SEQUENCE 1136 AA; 126066 MW; AD812130 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
  SUBMITTED
                                                                                STRAIN-WT3;
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                        PASENTSIS K., PAULO N., DUFNER M., KREISL P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PHY1_CERPU
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                                                                                                           REVISIONS TO C-TERMINAL
                                                                                                                                                                                         chain reaction."
                                                                                                                                                                                                               phytochrome gene in the moss
                                                                                                                                                                                                                                          THUEMMLER F., BEETZ A., RUEDIGER W.; "Phytochrome in lower plants. Detect
                                                                                                                                                                                                                                                                                         SEQUENCE OF 49-538 FROM MEDLINE; 91085543.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. MEDLINE; 93099252.
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                                                                                                                                                          LETT. 275:125-129(1990)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EPYLGLHYPATDIPQASRFLFMKNRVRMICDCCAPPVNVIQDKRLRQPLSLCGSTLRAPH 334
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  (FEB-1997) TO
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                                                 DITTRICH P., ALGARRA P.,
EMBL/GENBANK/DDBJ DATA BANKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 996; DB 1; L
Pred. No. 7.13e-219;
28; Mismatches 24;
                                                                                                                                                                                                               Ceratodon
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Ceratodon purpureus using the polym
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                                                                                                                                                                                                                                                                                                                                                                                                of the moss Ceratodon ated protein kinase.";
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                                                       THUEMMLER
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DOMAIN
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PFAM; PF00360; phytochrome; 1.
PFAM; PF00989; PAS; 1.
HSSP; P11362; 1FGI.
TRANSCRIPTION REGULATION; PHOT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; U87632; G1839248;
EMBL; X17084; G296091; I
PIR; S12966; S12966.
PIR; S27396; S27396.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
PROSITE; PS00245; PHYTOCHROME_L; 1.
PROSITE; PS50046; PHYTOCHROME_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               <del>-</del> -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TRANSCRIPTION REGULATION; PHOTORECEPTOR; PHYTOCHROME; CHRO TRANSFERASE; SERINE/THREONINE-PROTEIN KINASE; ATP-BINDING. DOMAIN 1 778 CHROMOPHORE BINDING DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
  172
                                                     379
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                                                                                                                                                                                                                                                                                                                                                                 199 KLAARAITRLQALPGGDIELLCDTIVEEVRELTGYDRVMAFKFHEDEHGEVVAEIRRMDL
                                                                                                                                                                                                           61
                                                                                                                                                                                                                                                                                                              1 KLAVRAISRLQSLPGGDIGALCDTVVEDVQRLTGYDRVMVYQFHEDDHGEVVSEIRRSDL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FUNCTION: REGULATORY PHOTORECEPTOR WHICH EXISTS IN TWO FORMS THAT ARE REVERSIBLY INTERECONVERTIBLE BY LIGHT: THE PR FORM THAT ABSORBS MAXIMALLY IN THE RED REGION OF THE SPECTRUM AND THE PFE FORM THAT ABSORBS MAXIMALLY IN THE FAR-RED REGION. PHOTOCONVERSION OF PR IN PFE INDUCES AN ARRAY OF MORPHOGENIC RESPONSES, WHEREAS RECONVERSION OF PR TO PR CANCELS THE INDUCTION OF THOSE RESPONSES. PFR CONTROLS THE EXPRESSION OF A NUMBER OF NUCLEAR GENES INCLUDING THOSE ENCODING THE SMALL SUBUNIT OF RIBULOSE-BISPHOSPHATE CARBOXYLASE, CHLOROPHYLL A/B BINDING PROTEIN, PROTOCHLOROPHYLLIDE REDUCTASE, RRNA, ETC. IT ALSO CONTROLS THE EXPRESSION OF TROLS THE EXPRESSION OF THOSE NUMBER OF NUCLEAR GENES INCLUDING THESE RECONTROLS THE EXPRESSION OF TS OWN GENE(S) IN A NEGATIVE FEEDBACK FASHION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUBUNIT: HOMODIMER.
SUBCELLULAR LOCATION: LOCATED IN A FIXED POSITION CLOSE PLASMA MEMBRANE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PTM: CONTAINS ONE COVALENTLY LINKED SIMILARITY: IN THE C-TERMINAL, WITH DOMAINS OF SER/THR-PROTEIN KINASES.
                                                                                                                                                                                                           EPYMGLHYPATDIPQASRFLLMKNRVRLIADCYASPVKLIQDPDIRQPVSLAGSTLRAPH 318
  CEFLMQAFGLQLQMELQLASQLAEK
                                                  CEFLMQVFGMQLNLHVELAAQLREK
                                                                                                        GCHTQYMANMGSVASLALAIVVKGKD--S--S----KLWGLVVGHHCSPRYVPFPLRYA
                                                                                                                                                      GCHAQYMGNMGSIASLYMAVIINDNEEYSRGAIQRGRKLWGLVVCQHTSPRTVPFPLRSV 378
                                                                                                                                                                                                                                                                                                                                                                                                            ch 67.6%;
1 Similarity 64.4%;
132; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 986;
Pred. No. 2.
                                                                                                                                                                                                                                                                                                                                                                                                                    38;
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ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
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     196
                                                  403
                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 1;
.85e-21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TETRAPYRROLE CHROMOPHORE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                    26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 1307;
                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CHROMOPHORE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 restrictions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL outstation
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in no way
r commercial
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RESULT ID PI

LT 15 PHY_MOUSC

STANDARD;

PRT;

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Best Local Similarity 64.4%;
                                                                                                                                                                                                                                                                      Matches
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01-FEB-1994 (REL.
01-NOV-1997 (REL.
01-NOV-1997 (REL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WINANDS A. WAGNER G., MARX S., SCHNEIDER-POETSCH H.A.;
WINANDS A. WAGNER G., MARX S., SCHNEIDER-POETSCH H.A.;
"Partial nucleotide sequence of phytochrome from the zygnematophycean green alga Mougeotia.";
green alga Mougeotia.";
"PARTIALLY IN TERCONVERTIBLE BY LIGHT: THE PR FORM THAT INTERCONVERTIBLE BY LIGHT: THE PR FORM THAT ABSORBS MAXIMALLY IN THE RED REGION OF THE SPECTRUM AND THE PER FORM THAT ABSORBS MAXIMALLY IN THE FAR-RED REGION. PHOTOCONVERSION OF PR IN PER INDUCES AN ARRAY OF MORPHOGENIC RESPONSES, WHEREAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
WINANDS A., WAGNER G.;
SUBMITTED (JUL-1996) TO EMBL/GENBANK/DDBJ DATA BANKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOUGEOTIA SCALARIS (HASSEL).
EUKARYOTA; VIRIDIPLANTAE; STREPTOPHYTA; CHAROPHYTA; ZYGNEMATALES;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PHYTOCHROME.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZYGNEMATACEAE; MOUGEOTIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; X95550; E221402; -.
EMBL; S52048; G262811; -.
PROSITE: PS00245; PHYTOCHROME_1;
PROSITE: PS50046; PHYTOCHROME_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                         TRANSCRIPTION REGULATION; PHOTORECEPTOR; PHYTOCHROME; CHROMOPHORE.
BINDING 325 325 CHROMOPHORE OF SIMILARITY).

CONFLICT 342 342 S -> C (IN REF. 2).

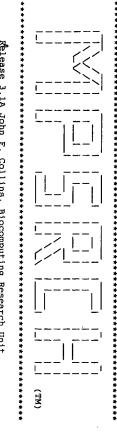
CONFLICT 381 381 R -> H (IN REF. 2).

CONFLICT 399 399 V -> A (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   PFAM; PF00360; phytochrome; PFAM; PF00512; signal; 1. PFAM; PF00989; PAS; 2.
                                                                                                                                                                                                                  204 KLAAKAISRLQSLPGGDICGLCDVVVEEVRELTGYDRVMAYKFHDDEHGEVVÄEIRRSDL 263
384 CEFIMQVFGLQLNMEVELAAQHREK 408
                                                      121
                                                                                                                                                               264
                                                                                                                           61
                                                                                                                                                                                                   1 KLAVRAISRLQSLPGGDIGALCDTVVEDVQRLTGYDRVMVYQFHEDDHGEVVSEIRRSDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUBUNIT: HOMODIMER.
PTM: CONTAINS ONE COVALENTLY LINKED TETRAPYRROLE CHROMOPHORE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RECONVERSION OF PFR TO PR CANCELS THE INDUCTION OF THOSE RESPONSES. PFR CONTROLS THE EXPRESSION OF A NUMBER OF NUCLEAR GENES INCLUDING THOSE ENCODING THE SMALL SUBUNIT OF RIBULOSE-BISPHOSPHATE CARBOXYLASE, CHLOROPHYLL A/B BINDING PROTEIN, PROTOCHLOROPHYLLIDE REDUCTASE, RRNA, ETC. IT ALSO CONTROLS THE EXPRESSION OF ITS OWN GENE(S) IN A NEGATIVE FEEDBACK FASHION.
                                                                                                                        GCHTQYMANMGSVASLALAIVVKG-KD-SS---
                                                                                        GCHTQYMMNMGSTASLVMSVTINDTNEIAGGPGMKGRKLWGLIVCHHSTPRHIPFPIRSA 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 93117305
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342 3
381 3
399 3
1124 AA;
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35,
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LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                             123923 MW;
                                                                                                                                                                                                                                                                    Score 977; DB 1; Length 1124; Pred. No. 6.23e-214; 31; Mismatches 33: Thirle
                                                                                                                                                                                                                                                                                                                                             CFDC29F3 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (See http://www.isb-sib.ch/announce/
                                                          KLWGLVVGHHCSPRYVPFPLRYA 171
                                                                                                                                                                                                                                                                          9;
                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                      60
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Qy 172 CEFLMQAFGLQLQMELQLASQLAEK 196

Search completed: Mon Sep 13 14:23:48 1999 Job time: 17 secs.

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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Tabular output not generated. Mon Sep 13 14:24:04 1999; MasPar time 14.69 Seconds 728.410 Million cell updates/sec

Title: Description: Perfect Score: >US-09-272-809-9 (1-196) from US09272809.pep 1458

Sequence: 1 KLAVRAISRLQSLPGGDIGA.....QAFGLQLQMELQLASQLAEK 196

Scoring table: PAM 150 Gap 11

Searched:

Post-processing:

179066 segs, 54579741 residues

Minimum Match 0% Listing first 45 summaries

Dátabase: sptremb19

1:sp_archea 2:sp_bacteria 3:sp_fungi 4:sp_human 5:sp_invertebrate 6:sp_mammal 7:sp_mhc 8:sp_organelle 9:sp_phage 10:sp_plant 11:sp_rodent 12:sp_unclassified 13:sp_vertebrate 14:sp_virus

Statistics: Mean 43.967; Variance 68.271; scale 0.644

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

20	1 6	17	16	15	14	13	12	11	10	9	8	7	6	G	4	ω	N	_	Result	•
996 996	1005	1011	1019	1026	1030	1030	1031	1033	1038	1039	1044	1045	1047	1056	1085	1087	1133	1157	Score	
68.8	68.9	69.3	69.9	70.4	70.6	70.6	. 70.7	70.9	71.2	71.3	71:6	71,7	71.8	72.4	74.4	74.6	77.7	79.4	Query Match	de
164 190	220	192	1142	198	1121	1118	191	193	1140	1164	195	193	197	196	197	1039	1130	1135	Length	
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P93123 P93170	Q41333	024278	Q40263	P93524	024446	080419	024069	024055	082148	023472	004809	004762	004789	024404	004779	P93527	024380	024117	ID	
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1.03e-227 7.70e-226	2.99e-228	7.38e-230	5.30e-232	7.04e-234	5.95e-235	5.95e-235	3.21e-235	9.33e-236	4.25e-237	2.29e-237	1.04e-238	5.63e-239	1.64e-239	6.28e-242	1.02e-249	2.95e-250	1.25e-262	4.28e-269	Pred. No.	

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4 4 5 4	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	21
753 746	753	757	759	763	768	770	773	803	804	815	839	850	885	888	898	959	959	965	980	984	987	990	996
51.6 51.2	51.6	51.9	52.1	52.3	52.7	52.8	53.0	55.1	55.1	55.9	57.5	58.3	60.7	60.9	61.6	65.8	65.8	66.2	67.2	67.5	67.7	67.9	68.3
190 10 190 10		215 10				190 10				193 10					200 10			186 10		187 10		221 10	
0 Q40747 0 009235		0 022569	0 004412						0 Q40756	0 004413				0 009240				0 024065				0 Q41332	0 Q40917
PHYTOCHROME (FRAGMENT) PHYTOCHROME (FRAGMENT)	PHYTOCHROME (FRAGMENT)	_	PHYTOCHROME (FRAGMENT)	PHYTOCHROME E (FRAGMEN	PHYTOCHROME (FRAGMENT)	PHYTOCHROME (FRAGMENT)	PHYTOCHROME (FRAGMENT)	ш.	PHYTOCHROME (FRAGMENT)	PHYTOCHROME (FRAGMENT)		PHYTOCHROME A.	PHYTOCHROME (FRAGMENT)	PODOCARPUS NERIIFOLIUS		PHYTOCHROME C.	PHYTOCHROME E (FRAGMEN	_	유 (PHYTOCHROME E (FRAGMEN	PHYTOCHROME E (FRAGMEN	PHYTOCHROME B1 (FRAGME	PHYTOCHROME (FRAGMENT)
3.47e-161 2.44e-159	3.47e-161	3.05e-162	9.03e-163	7.93e-164	3.78e-165	1.12e-165	1.80e-166	2.07e-174	1.13e-174	1.37e-177		٠	•	5.42e-197		•	6.12e-216			1.26e-222	٠	3.11e-224	7.70e-226

ALIGNMENTS

ργ	쿬	Qγ	ДD	Qy	Дb	Qy	g	# B O	Š	KW	DR	DR S	g R	DR	RL	RA	공;	R R	8	8	2 6) C	B	Ŋ,	313	۸	RESULT
EFLMQAFGLQLQMELQLASQLAEK	397 FETMOAFGTOLNMETOLAGOTGER 420		EEAVGGR	61 EPYLGLHYPATDIPQAARFLFKQNRVRMICDCNATPVKVVQSEELKRPLCLVNSTLRAPH 120	277 EPYIGLHYPATDIPQASRFLFKQNRVRMIVDCHATPVRVVQDESLMQPLCLVGSTLRAPH 336		217 KLAVRAISHLQSLPGGDVKILCDTVVESVRELTGYDRVMVYKFHEDEHGEVVAESKRPDL 276	Query Match 79.4%; Score 1157; DB 10; Length 1135; Best Local Similarity 77.5%; Pred. No. 4.28e-269; Matches 158; Conservative 25; Mismatches 13; Indels 8; Gaps 2;	SEQUENCE 1135 AA; 125810 MW; BB76B292 CRC32;	PHYTOCHROME.	DEAM: DE00989: DAS: 2	PFAM; PF00512; signal; 1.	PROSITE; PSUU245; PHYTOCHROME_1; 1.	EMBL; Y14676; E339604; -	DDBJ DATA BANKS.	HUDSON M.E., ROBSON P.R.H., KRAEPIEL Y., CABOCHE M., SMITH H.;	STRAIN=CV. PBH1D; TISSUE=LEAF;	SPOTTENCE ERON N A	ASTERIDAE; SOLANANAE; SOLANALES; SOLANACEAE; NICOTIANA.	EUPHYLLOPHYTES; SPERMATOPHYTA; MAGNOLIOPHYTA; EUDICOTYLEDONS;	RIKARYOTA: VIRIDIPLANTAF: STREETODHYTA: EMBRYODHYTA: TRACHEODHYTA:	CHICA.	PHYTOCHROME B.	01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)	1998 (TREMBLREL. 05, CREAT		O24117 DEELIMINARY: DET 1135 AA

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RESULT RE
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Best Local S
Matches 15
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O24380;
O1-JAN-1998
O1-JAN-1998
O1-NOV-1998
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SOLANUM TUBEROSUM (POTATO).

EUKARYOTA; VIRIDIPLANTAE; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA;

EUPHYLLOPHYTES; SPERMATOPHYTA; MAGNOLIOPHYTA; EUDICOTYLEDONS;

EUPHYLLOPHYTES; SOLANANE; SOLANALES; SOLANACEAE; SOLANUM.
                                                                                                                                                                                                                                                                                                                    P93527
P93527;
  CHILDS
MORGAN
                                                                                                                                                                                                                            01-MAY-1997 (TREMBLREL.
01-MAY-1997 (TREMBLREL.
01-JAN-1999 (TREMBLREL.
PHYTOCHROME B (FRAGMENT)
                                                                                                                                    SORGHUM BICOLOR MILO (SORGHUM).
EUKARYOTA; VIRIDIPLANTAE; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA;
EUPHYLLOPHYTES; SPERMATOPHYTA; MAGNOLIOPHYTA; LILIOPSIDA; POALES;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PFAM; PF00360; phytochrome; 1. PFAM; PF00512; signal; 1. PFAM; PF00989; PAS; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PLANT MOL. BIOL. 20:589-600(1992).
EMBL; Y14572; E333043; -.
PROSITE; PS00245; PHYTOCHROME_1; 1.
                                               STRAIN-CV. 58M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=CV. DESIREE;
MEDLINE; 93081720.
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                                                                  SEQUENCE FROM N.A.
                                                                                                                 POACEAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PHYTOCHROME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HEYER A., GATZ C.;
"Isolation and characterization of type B phytochrome.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                        172
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KLAVRAISHLQSLPGGDIKLLCDTVVESVRELTGYDRVMYKFHEDEHGEVVAESKRSDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GCHTQYMANMGSVASLALAIVVKGKD--S----S-KLWGLVVGHHCSPRYVPFPLRYA 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GCHAQYMANMGSIASLTLAVIINGNDEEAVGGGRNSMRLWGLVVGHHTSVRSIPFPLRYA 390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EPYIGLHYPATDIPQASRFLFKQNRVRMIVDCHATPVRVTQDESLMQPLCLVGSTLRAPH 330
                                                                                                                                                                                                                                                                                                                                                                                                                                        CEFLMQAFGLQLQMELQLASQLAEK 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EPYLGLHYPATDIPQAARFLFKQNRVRMICDCNATPVKVVQSEELKRPLCLVNSTLRAPH
K.L., MILLER P.W., MULLET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ch 77.7%;
l Similarity 77.1%;
158; Conservative
                                                                                                                 SORGHUM.
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(TREMBLREL.)
(TREMBLREL.)
E B.
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                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
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                                                                                                                                                                                                                                                  03, CREATED)
03, LAST SEQUENCE UPDATE)
09, LAST ANNOTATION UPDATE)
                     CORDONNIER-PRATT M.M.,
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LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 1133; DB 10;
Pred. No. 1.25e-262;
23; Mismatches 15;
                                                                                                                                                                                                                                                                                                                                              PRT;
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                     L.H.,
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Matches 15
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Best Local 9
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O04779;
O1-JUL-1997 (TREMBLREL. C
O1-JUL-1997 (TREMBLREL. C
O1-JAN-1999 (TREMBLREL. C
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NON_TER
SEQUENCE
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CARMICHAELIA SP. 'LAVIN 6201'.

CARMICHAELIA SP. 'LAVIN 6201'.

EUKARYOTA; VIRIDIPLANTAE; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA;

EUPHYLLOPHYTES; SPERMATOPHYTA; MAGNOLIOPHYTA; EUDICOTYLEDONS; ROSI

EUPHYLLOPHYTES; SPERMATOPHYTA; CARMICHAELIA.
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PHYTOCHROME.
NON_TER
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EMBL; U56730; G1800217; -.
PROSITE; PS00245; PHYTOCHROME_1; 1.
PFAM; PF00360; phytochrome; 1.
PFAM; PF00512; Signal; 1.
PFAM; PF00989; PAS; 2.
PFAM; PF00989; PAS; 2.
PFAM; PF00989; PAS; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                    U1-JUL-1997 (TREMBLREL. 04, 01-JUL-1997 (TREMBLREL. 04, 01-JAN-1999 (TREMBLREL. 09, PHYTOCHROME E (FRAGMENT).
                                                                                                                                                                                                                                                                                          LAVIN M., ESHBAUGH E., HU J.-M., AM. J. BOT. 85:412-433(1998). EMBL; U78839; G1711068; -.
                                                                                                                                                                                                                                                     PROSITE; PS00245; PHYTOCHROME_1; 1.
PFAM; PF00360; phytochrome; 1.
MENDEL; 14081; CARSS;2331;mn14081.
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155
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les 155; Conser
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                                                              KPVKVIQSEELRQPLCLVNSTLRSPHDCHTQYMANMGSIASLVMAVIVNGNDSTRLWGLL 120
                                                                                         YDRVMAYKFHEDDHGEVVSEIRRSDLEPYLGLHYPSTDIPQAARFLFKQNRVRMICDCHA
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                         VCHHSSPRYVPFPVRYACEFLMQAFGLQLYMEIQLASQMAEK 162
                                                 TPVKVVQSEELKRPLCLVNSTLRAPHGCHTQYMANMGSVASLALAIVVKGKDSSKLWGLV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EPYLGLHYPATDIPQASRFLFRQNRVRMIADCHATPVRVIQDPGMSQPLCLVGSTLRAPH 231
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VGHHCSPRYVPFPLRYACEFLMQAFGLQLQMELQLASQLAEK
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1 Similarity 84.0%;
136; Conservative
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197
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larity 74.5%;
Conservative
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LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDAT
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                                                                                                                                                  Score 1085; DB 10;
Pred. No. 1.02e-249;
18; Mismatches 8;
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Pred. No. 2.95e-250;
21; Mismatches 20;
                                                                                                                                                                                                       05DAFB24 CRC32;
                                                                                                                                                                                                                                                                                                                      MATHEWS
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196
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Best Local S
Matches 13
                                                                                                        Matches
                                                                                                                              Query Match
Best Local :
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01-JUL-1997
01-JAN-1999
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01-AUG-1998
01-NOV-1998
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ENTEROLOBIUM CYCLOCARPUM.
ENTEROLOBIUM CYCLOCARPUM.
EUKARYOTA; VIRIDIPLANTAE; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA;
EUPHYLLOPHYTAS; SPERMATOPHYTA; MAGNOLIOPHYTA; EUDICOTYLEDONS; ROSI
TYPKYTE: FARACEAE; MIMOSOIDEAE; ENTEROLOBIUM.
                                                                                                                                                                                                                                                       NON_TER
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EMBL; U78827; G1711080; -.

PROSITE: PS00245; PHYTOCHROME_1; 1

PFAM; PF00360; phytochrome; 1.

MENDEL; 14091; ENTCY;2331;mn14091.
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004789
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YDRVMAYKFHEDDHGEVVSEIRRSDLEPFFGLHYPATDIPQAARFLFKQNRVRMICDCHA
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132; Conser
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132; Conser
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197
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7 (TREMBLREL. 04, 09)
9 (TREMBLREL. 09, 09)
E E (FRAGMENT).
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196 AA;
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3 (TREMBLREL. (
5 (TREMBLREL. (
5 E (FRAGMENT)
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larity 81.5%;
Conservative
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larity 82.0%;
Conservative
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07,
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                                                                                               Score 1047;
Pred. No. 1.
19; Mismatc
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, LAST SEQUENCE UP
, LAST ANNOTATION
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LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 1056; DB 10;
Pred. No. 6.28e-242;
21; Mismatches 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OFB3DD8C CRC32;
                                                                                                                                                                                                                          E468A5CD CRC32;
                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MATHEWS
                                                                                           47; DB 10;
. 1.64e-239;
natches 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    197
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SHARROCK
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                                                                                                                                                        Length 197;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 196;
                                                                                               Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ROSIDAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                               Gaps
                                      60
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RESULT 8

ID 004809;

AC 004809;

AC 004809;

DT 01-JUL-1997

DT 01-AUG-1998

DT 01-JAN-1999

DE PHYTOCHROME 1

GN PHYE.

OS POECILANTHE 1

OC EUWARYOTA; V.

OC EUWARYOTA; V.

OC EUPHYLLOPHYTI

OC EUPHYLLOPHYTI

OC FABALES; FABI

RN [1]

OR SEQUENCE FROM

RA LAVIN M., ESI

RL AM. J. BOT. ESI

RL AM. J. BOT. ESI

DR EMBL; U78848

DR PEAM; FF00356

DR MENDEL; 1410:
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Best Local
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01-AUG-1998
01-JAN-1999
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NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         004762;
            LAVIN M., ESHBAUGH E., HU J.-M., AM. J. BOT. 85:412-433(1998).
EMBL; U78848; G3176484; PROSITE; PS00245; PHYTOCHROME_1; PFAM; PF00360; phytochrome; 1.
                                                                                            EUKARYOTA; VIRIDIPLANTAE; STREPTOPHYTA; EMBRYOPHYTA; TRACHBOP
EUPHYLLOPHYTES; SPERMATOPHYTA; MAGNOLIOPHYTA; EUDICOTYLEDONS;
FABALES; FABACEAE; PAPILIONOIDEAE; POECILANTHE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PHYE.
AUSTROSTEENISIA BLACKII.
BUSTROSTEENISIA BLACKII.
EUKARYOTA; VIRIDIPLANTAE; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPH
EUKARYOTA; VIRIDIPLANTAE; MAGNOLIOPHYTA; EUDICOTYLEDONS;
EUPHYLLOPHYTES; SPERMATOPHYTA; MAGNOLIOPHYTA; EUDICOTYLEDONS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AM. J. BOT. 85:412-433(1998).
EMBL; U78843; G3176474; -.
PROSITE; PS00245; PHYTOCHROME_1;
                                                                        SEQUENCE FROM N.A.
                                                                                                                                 POECILANTHE FALCATA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LAVIN M., ESHBAUGH E., HU J.-1
AM. J. BOT. 85:412-433(1998).
EMBL; U78843; G3176474; -.
  MENDEL; 14101;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MENDEL; 14070
PHYTOCHROME.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PFAM; PF00360;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                             TSPRYVPFPVRYACEFLMQAFGLQLYMEIQLASQMAEK
                                                                                                                                                                                                                                                                                                                                                          NPVKVIQSEESRQPLCLVNSTLRSPHQCHAQYMENMGSIASLVMAVIVNGNDTTKLWGLL
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                                                                                                                                                                                                                                                                                                                                                                                                         ch 71.7%;
l Similarity 83.5%;
l32; Conservative
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193
193
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G) (TREMBLREL.
G) E (FRAGMENT)
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                                                                                                                                                       (FRAGMENT).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     phytochrome; 1.
AUSb1; 2331; mn14070.
  POEfa; 2331; mn14101
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22073
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                                                                                                                                                                  CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                       Score 1045; DB 10;
Pred. No. 5.63e-239;
17; Mismatches 9;
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LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                 PRT;
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                                                            MATHEWS
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                                                            SHARROCK
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                                                                                                                                                                                                                                                                                                                                                                                                                               Length 193;
                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                   TRACHEOPHYTA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TRACHEOPHYTA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R.A.;
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                                                                                                          ROSIDAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ROSIDAE;
                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RP SEQUENCE FROM N.A.

RY MEDLINE; 9812113.

RA BEYAN M., BANCROFT I., BENT E., LOVE K., GOODMAN H., DEAN C.,

RA BEYAN M., BANCROFT I., BENT E., LOVE K., GOODMAN H., DEAN C.,

RA RIDLEY P., HUDSON S.A., PATEL K., MURPHY G., PIFFANELLI P., WEDLER H.,

RA RIDLEY P., HUDSON S.A., PATEL K., MURPHY G., PIFFANELLI P., WEDLER H.,

RA WEDLER E., WAMBUTT R., WEITZENEGGER T., POHL T.M., TERRYN N.,

RA AUBORG S., GY I., KREIS M., LAO N., KAVANAGH T., HEMPEL S., KOTTER P.,

RA AUBORG S., GY I., KREIS M., LAO N., KAVANAGH T., HEMPEL S., KOTTER P.,

RA AUBORG S., GY I., KREIS M., LAO N., KAVANAGH T., HEMPEL S., KOTTER P.,

RA AUBORG S., GY I., KREIS M., LAO N., FUNK B., MUELLER-AUER S.,

RA AUBORG S., GY I., KREIS M., LAO N., FUNK B., MUELLER-AUER S.,

RA VOUKELATOU E., MILIONI D., HATZOPOULOS P., PIRAVANDI E., OBERMAIER B.,

RA VOUKELATOU E., MILIONI D., HATZOPOULOS P., PIRAVANDI E., OBERMAIER B.,

RA VOUKELATOU E., MILIONI D., HATZOPOULOS P., PIRAVANDI E., OBERMAIER B.,

RA HILBERT H., DUESTERHOFT A., MOORES T., JONES J.D.G., ENEMA T.,

RA ALME K., BENES V., RECHMAN S., ANSORGE W., COOKE R., BERGER C.,

RA ALME K., BENES V., RECHMAN S., ANSORGE W., COOKE R., BERGER C.,

RA ALME K., BENES V., RECHMAN S., ANSORGE W., COOKE R., BERGER C.,

RA ALMER S., BOOK OF CONTIGUOUS SEQUENCE FROM Chromosome 4 of

RT ALADIADSIS OF CONTIGUOUS SEQUENCE FROM Chromosome 4 of

NATURE 391:485-488(1998).
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Best Local Similarity 83.1%;
Matches 133; Conservative
                                                                                                                                                                                                                      Query Mat&h
Best Local Similarity
                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     023472
023472;
01-JAN-1998
01-JAN-1998
01-NOV-1998
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NON_TER
NON_TER
SEQUENCE 1
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EUKARYOTA; VIRIDIPLANTAE; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA;
EUPHYLLOPHYTES; SPERMATOPHYTA; MAGNOLIOPHYTA; EUDICOTYLEDONS; ROSIDAE;
CAPPARALES; BRASSICACEAE; ARABIDOPSIS.
                                                                                                                                                                                                                                                                                                                                                                        PFAM; PF00360; phytochrome; PFAM; PF00512; signal; 1. PFAM; PF00989; PAS; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; z97340; E326982; -. PROSITE; PS00245; PHYTOCHROME_1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUBMITTED
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EU ARABIDOPSIS SEQ
                                                                                                                                                                                                                                                                                                                     SEQUENCE
299 EPYIGLHYPATDIPQASRFLFKQNRVRMIVDCYASPVRVVQDDRLTQF1CLVGSTLRAPH 358
                                                                                                     239 KLAVRAISHLQSLPSGDIKLLCDTVVESYRDLTGYDRVMYYKFHEDEHGEVVAESKRNDL 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        157
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                                                                  1 KLAVRAISRLQSLPGGDIGALCDTVVEDVQRLTGYDRVMVYQFHEDDHGEVVSEIRRSDL 60
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(TREMBLREL.
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                                                                                                                                                                                             Conservative
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-1997) TO EMBL/GENBANK/DDBJ
                                                                                                                                                                                                                      71.3%;
71.6%;
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Pred.
18; M
                                                                                                                                                                                                                                                                                                                  WW;
                                                                                                                                                                                                                      Score 1039; DB 10;
Pred. No. 2.29e-237;
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LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
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. No. 1.04e-238;
Mismatches 9;
                                                                                                                                                                                                                                                                                                                  994EB82E CRC32;
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                                                                                                                                                                                                                                                   Length 1164;
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Best Local Similarity 71.0%;
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082148;
082148;
01-NOV-1998
01-NOV-1998
01-NOV-1998
                                                                        MILLETTIA DURA.
EUKARYOTA; VIRIDIPLANTAE; STREPTOPHYTA; EMBRYC
EUPHYLLOPHYTES; SPERMATOPHYTA, MAGNOLIOPHYTA;
FABALES; FABACEAE; PAPILIONOIDEAE; MILLETTIA.
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EMBL; AB016232; D1034746; -.
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EUKARYOTA; VIRIDIPLANTAE; STREPTOPHYTA; EMBRYOPHYTA;
EUPHYLLOPHYTES; FILICOPHYTA; FILICOPSIDA; FILICALES;
SEQUENCE FROM N.A.
LAVIN M., ESHBAUGH E., HU J.-M.,
AM. J. BOT. 85:412-433(1998).
                                                                                                                                                                                                HYE
                                                                                                                                                                                                                       PHYTOCHROME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE 1140 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NOZUE K., FUKUDA S., KANEGAE T., WADA M.; "Isolation of a second phytochrome cDNA f
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PHYTOCHROME
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LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
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Pred. No. 4.25e-237;
25; Mismatches 24;
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                                                                                                                        EMBRYOPHYTA; TRACHEOP PHYTA; EUDICOTYLEDONS;
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                         SHARROCK R.A.
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                                                                                                                                            TRACHEOPHYTA;
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                                                                                                                        ROSIDAE;
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Best Local Similarity
Matches 133; Conser
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Best Local
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D30419;
O80419;
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O1-NOV-1998
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PHYTOCHROME.
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LAVIN M., ESHBAUGH E., HU J.-M., s
AM. J. BOT. 85:412-433(1998).
EMBL; AF004786; G3176521; -
PROSITE; PS00245; PHYTOCHROME_1;
PROSITE: PS00245; PHYTOCHROME_1;
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EUKARYOTA; VIRIDIPLANTAE; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA;
EUPHYLLOPHYTES; SPERMATOPHYTA; MAGNOLIOPHYTA; EUDICOTYLEDONS; ROSI
FABALES; FABACEAE; PAPILIONOIDEAE; MILLETTIA.
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PHYTOCHROME E (FRAGMENT).
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PROSITE; PS00245; PHYTOCHROME_1;
PFAM; PF00360; phytochrome; 1.
PHYTOCHROME.
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                                                                                                                                                                          QSEELRQPLCLVNSTLRSPHVCHTQYMANMGSIASLVMAIIVNGNDKTRLWGLLVCHHTS 120
                                                                                                                                                                                                                                                                                                                                        YQFHEDDHGEVVSEIRRSDLEPYLGLHYPATDIPQAARFLFKQNRVRMICDCNATPVKVV
                                                                                                                                                                                                                                                                                                                                                           YKFHEDDHGEVVSEIRRSDLEPYLGLHYPATDIPQASRFLFKQNRVRMICDCHAKPVKVI 60
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                  SEQUENCE UPDATE)
ANNOTATION UPDAT
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No. 9.
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HUGHES J.E., LA
PLANT PHYSIOL.
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024446;
024446;
01-JAN-1998
01-JAN-1998
01-NOV-1998
                                                                                                                                                  PASENTSIS K., PAULO N., DITTRICH P., ALGARRA P., SUBMITTED (OCT-1996) TO EMBL/GENBANK/DDBJ DATA BI EMBL; U72993; G1674478; -
EMBL; U72993; G1674478; -
PROSITE; PS00245; PHYTOCHROME_1; 1.
PFAM; PF00350; PHYTOCHROME; 1.
PFAM; PF00512; signal; 1.
PFAM; PF00989; PAS; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CERATODON PURPUREUS (MOSS).
EUKARYOTA; VIRIDIPLANTAE; STREPTOPHYTA; EMBRYOPHYTA;
BRYIDAE; DICRANALES; DITRICHACEAE; CERATODON.
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ADIANTUM CAPILLUS-VENERIS (FERN).
EUKARYOTA; VIRIDIPLANTAE; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA;
EUPHYLLOPHYTES; FILICOPHYTA; FILICOPSIDA; FILICALES; ADIANTACEAE;
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WADA M., KANEGAE T.,
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                                                                                                    SEQUENCE
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Similarity 68.8%;
141; Conservative
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L. 112:446-446(1996).
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EMBL/GENBANK/DDBJ
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Carpet C

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RESULT 15

ID P93524;
AC P93524;
DT 01-MAY-1997 (TREMBLREL. 03, CREATED)
DT 01-MAY-1997 (TREMBLREL. 03, LAST SEQUENCE UPDATE)
DT 01-JAN-1999 (TREMBLREL. 03, LAST ANNOTATION UPDATE)
DE PHYTCCHROME E (FRAGMENT).

SOPHORA AFFINIS.
OC SUPHYLLOPHYTES; SPERMATOPHYTA; EMBRYOPHYTA; TR
OC EUPHYLLOPHYTES; SPERMATOPHYTA; MAGNOLIOPHYTA; EUDICOTYI
OC EUPHYLLOPHYTES; SPERMATOPHYTA; SOPHORA.
RN [1]
RN SEQUENCE FROM N.A.
[1]
RA LAVIN M. ESHBAUGH E., HU J.-M., MATHEWS S., SHARROCK R
AM. J. BOT. 85:412-433(1998).
DR LAVIN M. ESHBAUGH E., HU J.-M., MATHEWS S., SHARROCK R
RL AM. J. BOT. 85:412-433(1998).
DR EMBL; U78837; G171110;
DR MENDEL; 14177; SOPAf; 2331;mn14177.
DR MENDEL; 14177; SOPAf; 2331;mn14177.
FT NON_TER 198 198
SQ SEQUENCE 198 AA; 22571 MW; 2A95C345 CRC32;
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                                                                                                                                                                                                                                                                                                         Query Match 70.4%; Score 1026; DB 10; Best Local Similarity 81.0%; Pred. No. 7.04e-234; Matches 132; Conservative 19; Mismatches 11;
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EUKARYOTA; VIRIDIPLANTAE; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA;
EUFHYLLOPHYTES; SPERMATOPHYTA; MAGNOLIOPHYTA; EUDICOTYLEDONS; ROSIDAE;
FABALEŠ; FABACEAE; PAPILIONOIDEAE; SOPHORA.
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|CEFLMQAFGLQLQMELQLASQLAEK 196
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